Title: Modulating developmental pathways in plants.

The invention relates to a method to modulate plant growth or development by modifying genes in plants. The invention among others relates to modifying RKS genes or gene products as found in *Arabidopsis thaliana* or other plants. The different domains of RKS gene products essentially have the following functions: The first domain of the predicted protein structure at the N-terminal end consists of a signal sequence, involved in targeting the protein towards the plasma membrane. Protein cleavage removes this sequence from the final mature protein product (Jain *et al.* 1994, J. Biol. Chemistry 269: 16306-16310). The second domain consists of different numbers of leucine zipper motifs, and is likely to be involved in protein protein dimerization. The next domain contains a conserved pair of cystein residues, involved in disulphate bridge formation. The next domain consists of 5 (or in the case of RKS3 only 4) leucine rich repeats (LRRs) shown in a gray colour, likely to be involved in ligand binding (Kobe and Deisenhofer 1994, TIBS 19: 415-420). This domain is again bordered by a domain containing a conserved pair of cystein residues involved in disulphate bridge formation often followed by a serine / proline rich region. The next domain displays all the characteristics of a simgle transmembrane domain. At the predicted cytoplasmic site of protein a domain is situated with unknown function, followed by a domain with serine /threonine kinase activity (Schmidt *et al.* 1997, Development 124: 2049-2062, WO 01/29240). The kinase domain is followed by a domain with unknown function whereas at the C-terminal end of the protein part of a leucine rich repeat is positioned, probably involved in protein-protein interactions.

Plant homologs of the Arabidopsis RKS genes can be found by comparison of various plant database (see also Table 2) and comprise amongst others:

Y14600|SBRLK1|*Sorghum bicolor*
BF004020|BF004020|EST432518 KV1 *Medicago truncatata*
AW934655|AW934655|EST353547 tomato
AW617954|AW617954|EST314028 *L. pennellii*
AA738544|AA738544|SbRLK2 *Sorghum bicolor*
AA738545|AA738545|SbRLK3 *Sorghum bicolor*
BG595415|BG595415|EST494093 cSTS *Solanum tuberosa*
AI896277|AI896277|EST265720 tomato
BF643238|BF643238|NF002H05EC1F1045
AA738546|AA738546|SbRLK4 *Sorghum bicolor*
BE658174|BE658174|GM700005A20D5 Gm-r1070 *Glycine max*
BF520845|BF520845|EST458318 DSIL *Medicago truncata*
AC069324|AC069324|*Oryza sativa*
AW761055|AW761055|sl70d06.y1 Gm-c1027 *Glycine max*
BE352622|BE352622|WHE0425_G11_M21ZS Wheat
BG647340|BG647340|EST508959 HOGA *Medicago truncata*
AY028699|AY028699|*Brassica napus*
AW666082|AW666082|sk31h04.y1 Gm-c1028 *Glycine max*
AA738547|AA738547|SbRLK5 *Sorghum bicolor*
BG127658|BG127658|EST473220 tomato
L27821|RICPRKI|*Oryza sativa*
BG238468|BG238468|sab51a09.y1 Gm-c1043 *Glycine max*
BG441204|BG441204|GA__Ea0012C15f *Gossypium arbo.*
AW667985|AW667985|GA__Ea0012C15 *Gossypium arbore.*
AW233982|AW233982|sf32g05.y1 Gm-c1028 *Glycine max*
AP003235|AP003235|*Oryza sativa*
BF460294|BF460294|074A05 Mature tuber
AY007545|AY007545|*Brassica napus*
AC087544|AC087544|*Oryza sativa*
AB041503|AB041503|*Populus nigra*

The invention furthermore relates to modifying ELS genes or gene products or functional equivalents thereof which are for example derived from at least two different genes in the Arabidopsis genome. They show high homology on protein level

with the corresponding transmembrane RKS gene products. However, they lack a transmembrane domain while they do contain a signaling sequence at the N-terminal end. Therefore these proteins are thought to be positioned within vesicles within the plant cell or at the outside of the plasma membrane, within the cell wall of the plant cell. A number of homologs have been detected in other plant species, such as:

AF370543|AF370543|*Arabidopsis thaliana*
AF324989|AF324989|*Arabidopsis thaliana*
AV520367|AV520367|*Arabidopsis thaliana*
AV553051|AV553051|*Arabidopsis thaliana*
BF642233|BF642233|NF050C09IN1F1069
AW559436|AW559436|EST314484 DSIR *Medicago truncata*
BG456991|BG456991|NF099F02PL1F1025
AW622146|AW622146|EST312944 tomato
BF260895|BF260895|HVSMEf0023D15f *Hordeum vulgare*
BE322325|BE322325|NF022E12IN1F1088
BG414774|BG414774|HVSMEk0003K21f *Hordeum vulgare*
BE460627|BE460627|EST412046 tomato
BI204894|BI204894|EST522934 cTOS *Lycopersicon esculentum*
BI205306|BI205306|EST523346 cTOS *Lycopersicon esculentum*
BI204366|BI204366|EST522406 cTOS *Lycopersicon esculentum*
AW443205|AW443205|EST308135 tomato
AW031110|AW031110|EST274417 tomato
BI180080|BI180080|EST521025 cSTE *Solanum tuberosa*
BF644761|BF644761|NF015A11EC1F1084
AV526127|AV526127|*Arabidopsis thaliana*
AV556193|AV556193|*Arabidopsis thaliana*
BE203316|BE203316|EST403338 KV1 *Medicago truncatata.*
AW649615|AW649615|EST328069 tomato
BE512465|BE512465|946071E06
BI204917|BI204917|EST522957 cTOS *Lycopersicon esculentum*
BG590749|BG590749|EST498591
BG648725|BG648725|EST510344 HOGA *Medicago truncata*
BG648619|BG648619|EST510238 HOGA *Medicago truncata*
BG597757|BG597757|EST496435 cSTS *Solanum tuberosa*
AW221939|AW221939|EST298750 tomato
BE704836|BE704836|Sc01_
BG124409|BG124409|EST470055 tomato

BF051954|BF051954|EST437120 tomato
BG320355|BG320355|Zm03_05h01_*Zea mays*
AV526624|AV526624|*Arabidopsis thaliana*
AW933960|AW933960|EST359803 tomato
AW221278|AW221278|EST297747 tomato
BE405514|BE405514|WHE1212_C01_F02ZS Wheat
BG314461|BG314461|WHE2495_A12_A23ZS *Triticum*
BF258673|BF258673|HVSMEf0016G01f *Hordeum vulgare*
BG262637|BG262637|WHE0938_E03_I06ZS Wheat
AW030188|AW030188|EST273443 tomato
BG653580|BG653580|sad76b11.y1 Gm-c1051 *Glycine max*
BG319729|BG319729|Zm03_05h01_A Zm03_*Zea mays*
BF053590|BF053590|EST438820 potato
BE454808|BE454808|HVSMEh0095C03f *Hordeum vulgare*
BI075801|BI075801|IP1_21_D05.b1_A002
BE367593|BE367593|PI1_9_F02.b1_A002 *Sorghum bicolor*
2e-074 BF260080|BF260080|HVSMEf0021A22f *Hordeum vulgare*
BF627921|BF627921|HVSMEb0006I23f *Hordeum vulgare*
BG598491|BG598491|EST503391 cSTS *Solanum tuberosa*
AW038168|AW038168|EST279825 tomato
BG343258|BG343258|HVSMEg0005D23f *Hordeum vulgare*
AW925684|AW925684|HVSMEg0005D23 *Hordeum vulgare*
BG416093|BG416093|HVSMEk0009L18f *Hordeum vulgare*
AW683370|AW683370|NF011C09LF1F1069
BE420108|BE420108|WWS020.C1R000101 ITEC WWS Wheat
AW350720|AW350720|GM210009A10F4 Gm-r1021 *Glycine max*
AW616564|AW616564|EST322975 L. *Hirsutum trichome*
AW011134|AW011134|ST17B03 Pine
BF630746|BF630746|HVSMEb0013N06f *Hordeum vulgare*
AW926045|AW926045|HVSMEg0006C10 *Hordeum vulgare*
BE519800|BE519800|HV_CEb0021E12f *Hordeum vulgare*
BG343657|BG343657|HVSMEg0006C10f *Hordeum vulgare*
BG933682|BG933682|OV1_16_C09.b1_A002
BE433368|BE433368|EST399897 tomato
AW219797|AW219797|EST302279 tomato
BF629324|BF629324|HVSMEb0010N06f *Hordeum vulgare*
BE597128|BE597128|PI1_71_A07.g1_A002
AW220075|AW220075|EST302558 tomato
AW616639|AW616639|EST323050 L. *Hirsutum trichome*
BF645214|BF645214|NF032F11EC1F1094
AW924540|AW924540|WS1_70_H12.b1_A002

AI775448|AI775448|EST256548 tomato
AW983360|AW983360|HVSMEg0010F15f *Hordeum vulgare*
BF270171|BF270171|GA__Eb0007B13f *Gossypium arbor.*
BE919631|BE919631|EST423400 potato
AW037836|AW037836|EST279465 tomato
BF008781|BF008781|ss79h09.y1 Gm-c1064 *Glycine max*
BF254651|BF254651|HVSMEf0004K05f *Hordeum vulgare*
BE599797|BE599797|PI1_79_H01.g1_A002
BE599026|BE599026|PI1_86_E03.g1_A002
R89998|R89998|16353 Lambda-PRL2 *Arabidopsis*
BG841108|BG841108|MEST15-G02.T3 ISUM4-TN *Zea mays*
AW307218|AW307218|sf54c07.y1 Gm-c1009 *Glycine max*
AI496325|AI496325|sb05c09.y1 Gm-c1004 *Glycine max*
AJ277703|ZMA277703|*Zea mays*
AL375586|CNS0616P|*Medicago truncatula* EST
AW350549|AW350549|GM210009A10A12 Gm-r1021 *Glycine max*
BE125918|BE125918|DG1_59_F02.b1_A002
BF053901|BF053901|EST439131 potato
BE921389|BE921389|EST425266 potato
BE597551|BE597551|PI1_71_A07.b1_
BE360092|BE360092|DG1_61_C09.b1_A002
BE660084|BE660084|491 GmaxSC *Glycine max*
AJ277702|ZMA277702|*Zea mays*

The invention also relates to modifying SBP/SPL gene or products which represent a family of transcription factors with a bipartite nuclear localization signal (The SQUAMOSA PROMOTER-BINDING PROTEIN-LIKE (SBP/SPL) gene family of *Arabidopsis thaliana*, Columbia ecotype). Upon activation (probably by RKS mediated phosphorylation, the bipartite nuclear localization signal becomes linear and available for the nuclear translocation of the protein. Within the plant nucleus, the transcription factor regulates transcription by interaction with specific promoter elements. . In *Arabidopsis thaliana*, this family is represented by at least 16 different members (see following list). In many other plant species, we also identified members of this transcription factor family (See list on page 7).

Functional interaction between RKS and SBP proteins was shown by studies in transgenic tobacco plants in which SBP5 and RKS0 were both overexpressed under the control of an enhanced 35S promoter (data not shown). At the tip of double overexpressing plants, embryo structures appeared whereas in the SBP5 overexpressing plants alone or the RKS0 overexpressing plants alone no phenotype was detectable at the root tips of transgenic tobacco plants. These results show that both RKS and SBP proteins are involved together in a signalling cascade, resulting in the reprogramming of developmental fate of a determined meristem. (ref. dissertation: http://www.ub.uni-koeln.de/ediss/archiv/2001/11w1204.pdf; Plant Journal 1997: 12, 2 367-377; Mol. Gen. Genet. 1996: 250, 7-16; Gene 1999, 237, 91-104, Genes and Development 1997: 11, 616-628), Proc. Natl. Acad. Sci. USA 1998: 95, 10306-10311; The Plant Journal 2000: 22, 523-529; Science 1997: 278, 1963-1965; Plant Physiol. Biochem. 2000: 38, 789-796; Cell 1996: 84, 61-71; Annu. Rev. Plant Physiol. Plant Mol. Biol. 1999: 50, 505-537

name	genetic code
ATSPL1	At2g47070*
ATSPL2	At5g43270
ATSPL3	At2g33810*
ATSPL4	At1g53160*
ATSPL5	At3g15270
ATSPL6	At1g69170
ATSPL7	At5g18830
ATSPL8	At1g02065
ATSPL9	At2g42200*
ATSPL10	At1g27370*
ATSPL11	At1g27360*
ATSPL12	At3g60030
ATSPL13	At5g50570
ATSPL14	At1g20980
ATSPL15	At3g57920
ATSPL16	At1g76580

* annotation in database not complete and/or correct

In many other plant species, we identified members of this transcription factor family, plant homologs of the Arabidopsis SBP/SPL proteins are for example:

AB023037|AB023037|*Arabidopsis thaliana*
BG789832|BG789832|sae56b07.y1 Gm-c1051 *Glycine max*
BG123992|BG123992|EST469638 tomato
BG595750|BG595750|EST494428 cSTS *Solanum tuberosum*
AF370612|AF370612|*Arabidopsis thaliana*
BF728335|BF728335|1000060H02.x1 1000 - *Zea mays*
X92079|AMSBP2|*A.majus*
AW331087|AW331087|707047A12.x1 707 - Mixed adult... 128 *zea mays*
AJ011643|ATH011643|*Arabidopsis thaliana*
L34039|RICRMSOA|*Oryza sativa*
AJ011638|ATH011638|*Arabidopsis thaliana*
AJ011639|ATH011639|*Arabidopsis thaliana*
AJ132096|ATH132096|*Arabidopsis thaliana*
BF482644|BF482644|WHE2301-2304_A21_A21ZS Wheat
BF202242|BF202242|WHE0984_D01_G02ZS Wheat
BE057470|BE057470|sm58e10.y1 Gm-c1028 *Glycine max*
AJ011628|ATH011628|*Arabidopsis thaliana*
AJ011629|ATH011629|*Arabidopsis thaliana*
AJ011617|ZMA011617|*Zea mays*
AJ011637|ATH011637|*Arabidopsis thaliana*
AJ011622|AMA011622|*Antirrhinum majus*
AJ011621|AMA011621|*Antirrhinum majus*
AJ011635|ATH011635|*Arabidopsis thaliana*
AJ011623|AMA011623|*Antirrhinum majus*
BF650908|BF650908|NF098D09EC1F1076
AJ242959|ATH242959|*Arabidopsis thaliana*
Y09427|ATSPL3|*A.thaliana* mRNA
AJ011633|ATH011633|*Arabidopsis thaliana*
AW691786|AW691786|NF044B06ST1F1000
BE058432|BE058432|sn16a06.y1 Gm-c1016 *Glycine max*
AW728623|AW728623|GA__Ea0017G06 *Gossypium arbore.*
BG442540|BG442540|GA__Ea0017G06f *Gossypium arbo.*
AJ011626|ATH011626|*Arabidopsis thaliana*
AJ011625|ATH011625|*Arabidopsis thaliana*
AI993858|AI993858|701515182 A. *thaliana*
BG593787|BG593787|EST492465 cSTS *Solanum tuberosum*
BF634536|BF634536|NF060C08DT1F1065 Drought *Medicago*

BE806499|BE806499|ss59f10.y1 Gm-c1062 *Glycine max*
AW933950|AW933950|EST359793 tomato
AC008262|AC008262| *Arabidopsis*
B28493|B28493|T10A24TF TAMU *Arabidopsis thaliana*
AJ011644|ATH011644|*Arabidopsis thaliana*
AC018364|AC018364|*Arabidopsis thaliana*
AL092429|CNS00VLB|*Arabidopsis thaliana*
BE435668|BE435668|EST406746 tomato
BG097153|BG097153|EST461672 potato
BE440574|BE440574|sp47b09.y1 Gm-c1043 *Glycine max*
AI443033|AI443033|sa31a08.y1 Gm-c1004 *Glycine max*
U89496|ZMU89496|*Zea mays* liguleless1
AW433271|AW433271|sh54g07.y1 Gm-c1015 *Glycine max*
AW932595|AW932595|EST358438 tomato
AW096676|AW096676|EST289856 tomato
AJ011616|ZMA011616|*Zea mays*
AW036750|AW036750|EST252139 tomato
BF626329|BF626329|HVSMEa0018F24f *Hordeum vulgare*
AJ011614|ZMA011614|*Zea mays*
AJ011642|ATH011642|*Arabidopsis thaliana*
BE022435|BE022435|sm85h04.y1 Gm-c1015 *Glycine max*
X92369|AMSPB1|*A.majus*
AC015450|AC015450|*Arabidopsis thaliana*
AC079692|AC079692|*Arabidopsis thaliana*
AJ011632|ATH011632|*Arabidopsis thaliana*
AJ011631|ATH011631|*Arabidopsis thaliana*
BE455349|BE455349|HVSMEh0097E20f *Hordeum vulgare*
AJ242960|ATH242960|*Arabidopsis thaliana*
AJ011610|ATH011610|*Arabidopsis thaliana*
AJ132097|ATH132097|*Arabidopsis thaliana*
AL138658|ATT2O9|*Arabidopsis thaliana*
AJ011615|ZMA011615|*Zea mays*
BE499739|BE499739|WHE0975_ Wheat
AW398794|AW398794|EST309294 *L. pennellii*
AJ011618|ZMA011618|*Zea mays*
AW747167|AW747167|WS1_66_F11.b1_
AJ011577|ATH011577|*Arabidopsis thaliana*
AI992727|AI992727|701493410 *A. thaliana*
BE060783|BE060783|HVSMEg0013F15f *Hordeum vulgare*
BE804992|BE804992|ss34h10.y1 Gm-c1061 *Glycine max*
BE325341|BE325341|NF120H09ST1F1009

AC007369|AC007369|*Arabidopsis thaliana*
AJ011619|ZMA011619|*Zea mays*
BI099345|BI099345|IP1_37_H10.b1_A002
BI071295|BI071295|C054P79U *Populus*
AZ920400|AZ920400|1006019G01.y2 1006 -
AZ919034|AZ919034|1006013G02.x3 1006 -
BE805023|BE805023|ss35d09.y1 Gm-c1061 *Glycine max*
BG582086|BG582086|EST483824 GVN *Medicago truncata*
AJ011609|ATH011609|*Arabidopsis thaliana*
BE023083|BE023083|sm90e08.y1 Gm-c1015 *Glycine max*

Furthermore, the invention relates to modifying NDR-NHL-genes or gene products. All proteins belonging to this family contain one (and sometimes even more than one) transmembrane domain. *Arabidopsis* contains a large number of NDR-NHL genes, such as:
aad21459, aaf18257, aac36175, k10d20 (position 40852-41619), aad21460, cab78082, aad21461, aad42003, aaf02134, aaf187656, aaf02133, cab43430, cab88990, cab80950, aad25632, aaf23842, al163812, f20d21-35, t13m11-12, f1e22-7, t23g18, f5d14-4266, t32f12-16, f11f19-11, f11f19-12, f11f19-13, t20p8-13, f12k2, f23h14, k10d20-44043, k10d20-12, t19f11-6, t19f11-5, t10d17-10, f22o6-150, f3d13-5, m3e9-80, t25p22-30, mhf15-4, mhf15-5, mrn17-4, mlf18-9, mgn6-11994, mjj3-9667, f14f18-60, At1g17620 F11A6, At5g11890 , At2g27080 , At5g36970 , mlf18 , At1g65690 F1E22 , At4g01110 F2N1 , At2g35980 f11f19 , At4g01410 F3D13 , At1g54540 F20D21 , At2g46300 t3f17 , At5g21130 , At3g11650 T19F11 , At5g06320 MHF15 , At5g06330 MHF15 , At2g01080 f15b18 , At2g35460 t32f12 , At2g27260 f12k2 , At2g35970 f11f19 , At5g53730 MGN6 , At5g22870 MRN17 , At4g09590 , At3g54200 , At1g08160 T6D22 , At5g22200 , At3g52470 , At2g35960 f11f19 , At3g52460 , At5g56050 MDA7, At3g20590 K10D20 , At1g61760 T13M11 , At3g20600 K10D20 , At1g13050 F3F19 , At3g11660 T19F11 , At3g44220 , At1g64450 F1N19 , At3g26350 F20C19 C , At4g05220 , At5g45320 K9E15 , At4g23930 , At4g13270 , At4g39740 , At1g45688 F2G19 W , At5g42860 MBD2 , At1g32270 F27G20 , At4g30660 , At2g45430 f4123 , At4g30650 , At1g69500 F10D13

and

ndr1, At2g27080; T20P8.13, At5g21130, At1g65690, At5g36970,

At1g54540, At5g06320, At5g11890, At1g17620, At3g11650, At2g22180, At5g22870, At2g35980, At2g46300, At4g05220, At2g35460, At2g27260, At4g01410, At5g22200, At1g61760, At3g52470, At5g53730, At4g01110, At2g35960, At3g52460, At4g09590, At2g35970, At3g26350, At3g11660, At3g44220, At1g08160, At2g01080, At5g06330, At5g56050, At3g20600, NDR1, At3g54200, At3g20590, At4g39740, At1g32270 syntaxin, putative, At1g13050, At5g45320, At3g20610, At4g26490, At5g42860, At1g45688, At4g26820

NDR-NHL genes belong to a large family of which one of the first identified is the defence-associated gene HIN1 (Harpin-induced gene). HIN1 is transcriptionally induced by harpins and bacteria, that elicit hypersensitive responses in tobacco. It is thus believed that the genes of the invention also play arole in the hypersensitive reaction. Especially (see also chapter 8) since the genes of the invention bear relation to brassinoid-like responses and since brassinoid pathway compounds have been found to interact in this same defence system in plants. Other plant species also contain members of this large gene family, such as:

Plant homologs of the *Arabidopsis* NDR/NHL genes:

BG582276|BG582276|EST484016 GVN *Medicago truncata*
AV553539|AV553539|*Arabidopsis thaliana*
AC069325|AC069325|*Arabidopsis thaliana*
AV526693|AV526693|*Arabidopsis thaliana*
BG583456|BG583456|EST485208 GVN *Medicago truncata*
AW267833|AW267833|EST305961 DSIR *Medicago truncata*
BE997791|BE997791|EST429514 GVSN *Medicago truncata*
BG580928|BG580928|EST482657 GVN *Medicago truncata*
BF520916|BF520916|EST458389 DSIL *Medicago truncata*
AV544651|AV544651|*Arabidopsis thaliana*
AV543762|AV543762|*Arabidopsis thaliana*
AW559665|AW559665|EST314777 DSIR *Medicago truncata*
BG581012|BG581012|EST482741 GVN *Medicago truncata*
AV552164|AV552164|*Arabidopsis thaliana*
BE999881|BE999881|EST431604 GVSN *Medicago truncata*
AW031098|AW031098|EST274405 tomato

AI998763|AI998763|701546833 *A. thaliana*
AW219286|AW219286|EST301768 tomato
BE124562|BE124562|EST393597 GVN *Medicago truncata*
AV540371|AV540371|*Arabidopsis thaliana*
AV539549|AV539549|*Arabidopsis thaliana*
BG647432|BG647432|EST509051 HOGA *Medicago truncata*
BE434210|BE434210|EST405288 tomato
BG725849|BG725849|sae42g02.y1 Gm-c1051 *Glycine max*
AP003247|AP003247|Oryza sativa
BE348073|BE348073|sp11a11.y1 Gm-c1042 *Glycine max*
AW508383|AW508383|si40c06.y1 Gm-r1030 *Glycine max*
AI856504|AI856504|sb40b07.y1 Gm-c1014 *Glycine max*
BE556317|BE556317|sq01b07.y1 Gm-c1045 *Glycine max*
AA713120|AA713120|32681 *Arabidopsis*
AV541531|AV541531|*Arabidopsis thaliana*
AI894456|AI894456|EST263911 tomato
AW704493|AW704493|sk53g11.y1 Gm-c1019 *Glycine max*
AW219298|AW219298|EST301780 tomato
BF425685|BF425685|ss03c11.y1 Gm-c1047 *Glycine max*
AV422557|AV422557|*Lotus japonicus*
BE190816|BE190816|sn79a08.y1 Gm-c1038 *Glycine max*
BG580331|BG580331|EST482056 GVN *Medicago truncata*
AV423251|AV423251|*Lotus japonicus*
AI896088|AI896088|EST265531 tomato
AV413427|AV413427|*Lotus japonicus*
AV426656|AV426656|*Lotus japonicus*
AV416256|AV416256|*Lotus japonicus*
AL385732|CNS0690I|*Medicago truncatula*
AB016877|AB016877|*Arabidopsis thaliana*
AV419449|AV419449|*Lotus japonicus*
AI486269|AI486269|EST244590 tomato
AV411690|AV411690|*Lotus japonicus*
AV419925|AV419925|*Lotus japonicus*
AV418222|AV418222|*Lotus japonicus*
AV409427|AV409427|*Lotus japonicus*
AC005287|AC005287|*Arabidopsis thaliana*
AV426716|AV426716|*Lotus japonicus*
AV411791|AV411791|*Lotus japonicus*
BG351730|BG351730|131E12 Mature tuber
BG046452|BG046452|saa54b12.y1 Gm-c1060 *Glycine max*
AI781777|AI781777|EST262656 tomato

BE451428|BE451428|EST402316 tomato
AI772944|AI772944|EST254044 tomato
AI895510|AI895510|EST264953 tomato
AW030762|AW030762|EST274017 tomato
AW218859|AW218859|EST301341 tomato
BE203936|BE203936|EST396612 KV0 *Medicago truncata*
AV410289|AV410289|*Lotus japonicus*
AW032019|AW032019|EST275473 tomato
AW030868|AW030868|EST274158 tomato
AV421824|AV421824|*Lotus japonicus*
BG646408|BG646408|EST508027 HOGA *Medicago truncata*
AF325013|AF325013|*Arabidopsis thaliana*
AC007234|AC007234|*Arabidopsis thaliana*
AW217237|AW217237|EST295951 tomato
AC034257|AC034257|*Arabidopsis thaliana*
AW625608|AW625608|EST319515 tomato
AW031064|AW031064|EST274371 tomato
AF370332|AF370332|*Arabidopsis thaliana*
AB006700|AB006700|*Arabidopsis thaliana*
AW035467|AW035467|EST281205 tomato
AL163812|ATF14F18|*Arabidopsis thaliana*
AI896652|AI896652|EST266095 tomato
AI730803|AI730803|BNLGHi7970 Cotton
AW034775|AW034775|EST278811 tomato

The invention provides the insight that RKS proteins or functional equivalents thereof play part in a signaling complex (herein also called the RKS signaling complex) comprising molecules of RKS proteins, ELS (Extracellular Like SERK) proteins, NDR/NHL proteins and SBP/SPL (Squamosa Binding Protein) proteins, and the corresponding protein ligands (see for example table 3) whereby each of these proteins interplay or act in such a way that modifying genes, or modifying expression of genes, encoding ELS, RKS, NDR/NHL or SBP/SPL, proteins or said ligands may lead to functionally equivalent results (Figure 5. Two-hybrid interaction experiments have for example shown in vitro interaction between RKS 0 and NDR0/NHL28 and members of the SBP/SPL family. Here we show that in vivo the individual components of this signaling

complex are regulating identical processes, as based on functional genomics on transgenic plants, overexpressing or co-suppressing single components or combinations of components in this transmembrane signalling complex. ELS gene products are derived from at least two different genes in the Arabidopsis genome. They show high homology on protein level with the corresponding transmembrane RKS gene products.

However, they lack a transmembrane domain while they do contain a signalling sequence at the N-terminal end. Therefore these proteins are thought to be positioned within vesicles within the plant cell or at the outside of the plasma membrane, within the cell wall of the plant cell. A number of homologues have been detected in other plant species (see list on page 3). ELS proteins are involved in the heterodimerizing complex with the RKS transmembrane receptor at the outer membrane site. ELS molecules are either in competition or collaboration with RKS molecules involved in the high affinity binding of the ligand. The signal transmitted from the ligand onto the RKS proteins is then transporter over the membrane towards the N-terminal site of RKS protein, located on the other site of the membrane. The activation stage of the RKS molecule is changed, as a result of transphosphorylation by dimerizing receptor kinase dimerizing partners. Subsequently the signal is transmitted to other proteins, one family of such proteins is defined as the SBP/SPL family of transcription factors, the other family of proteins is represented by the NDR/NHL members.

The different obvious phenotypes created by modifying the RKS gene products could be effected by one process regulating all different effects in transgenic plants.

All the phenotypes observed can be effected by the process of brassinosteroid perception. In chapter 1, RKS genes are clearly involved in plant size and organ size. Loss of RKS expression results in a dwarf phenotype, similar as observed with brassinosteroid synthesis mutants. It was already known in literature that the phenotypes observed from modifying the

RKS genes are also observed when modifying the brassinosteroid pathway genes and/or their regulation, thereby altering the amount and nature of the brassinosteroids in plants. Literature which describes the phenotypic effects of modifying teh brassionosteroid pathway can, amogst others, be found in: Plant Journal 26: 573-582 2001; Plant Journal 1996 9(5) 701-713, genetic evidence for an essential role of brassinosteroids in plant development; J. Cell Biochem Suppl. 21a 479 (1995) ; Mandava 1988 Plant growth-promoting brassinosteroids, Ann. Rev. Plant. Physiol. Plant Mol. Biol. 39 23-52; Plant Physiol 1994 104: 505-513; Cell 85 (1996) 171-182; Clouse *et al.* 1993 J. Plant Growth Regul. 12 61-66; Clouse and Sasse (1998) Annu. Rev. Plant Physiol. Plant Mol. Biol 49 427-451; Sasse, Steroidal Plant Hormones. Springer-Verlag Tokyo pp 137-161 (1999).

It is thus believed, without being bound to any theory, that modification of the RKS genes will result in a modification of the brassinosteroid pathway, thereby giving the various phenotypes that are shown below.

"Functionally equivalent" as used herein is not only used to identify the functional equivalence of otherwise not so homologous genes encoding ELS, RKS, NDR/NHL or SBP/SPL proteins, but also means an equivalent gene or gene product of genes encoding ELS, RKS, NDR/NHL or SBP/SPL proteins in *Arabidopsis Thaliana*, e.g. identifying a homologue found in nature in other plants or a homologue comprising a deliberate nucleic acid modification, such as a deletion, truncation, insertion, or deliberate codon substitution which may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, and/or the amphipathic nature of the residues as long as the biological activity of the polypeptide is retained. Homology is generally over at least 50% of the full-length of the relevant sequence shown herein. As is well-understood, homology at the amino acid level is generally in terms of amino acid similarity or identity. Similarity allows for "conservative variation", i. e. substitution of one

hydrophobic residue such as isoleucine, valine, leucine or methionine for another, or the substitution of one polar residue for another, such as arginine for lysine, glutamic for aspartic acid, or glutamine for asparagine. Deliberate amino acid substitution may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, and/or the amphipathic nature of the residues as long as the biological activity of the polypeptide is retained. In a preferred embodiment, all percentage homologies referred to herein refer to percentage sequence identity, e.g. percent (%) amino acid sequence identity with respect to a particular reference sequence can be the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the reference sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, without considering any conservative substitutions as part of the sequence identity. Amino acid similarity or identity can be determined by genetic programs known in the art.

'Plant cell', as used herein, amongst others comprises seeds, suspension cultures, embryos, meristematic regions, callous tissues, protoplasts, leaves, roots, shoots, bulbs, gametophytes, sporophytes, pollen and microspores. A target plant to be modified according to the invention may be selected from any monocotyledonous or dicotyledonous plant species, such as for example ornamental plants, vegetables, arable crops etc. 'Dicotyledoneae' form one of the two divisions of the flowering plants or angiospermae in which the embryo has two or more free or fused cotyledons. 'Monocotyledoneae' form one of the two divisions of the flowering plants or angiospermae in which the embryo has one cotyledon. 'Angiospermae' or flowering plants are seed plants characterized by flowers as specialized organs of plant reproduction and by carpels covering the ovaries. Also included are gymnospermae. Gymnospermae are seed plants characterized by strobili as specialized organs for plant reproduction and by naked sporophylls bearing the male or female reproductive organs, for example woody plants. 'Ornamental'

plants are plants that are primarily in cultivation for their habitus, special shape, (flower, foliage or otherwise) colour or other characteristics which contribute to human well being indoor as cut flowers or pot plants or outdoors in the man made landscape, for example bulbous plant species like *Tulipa*, *Freesia*, *Narcissus*, *Hyacinthus* etc. 'Vegetables' are plants that are purposely selected or bred for human consumption of foliage, tubers, stems, fruits, flowers or parts of them and that may need an intensive cultivation regime. 'Arable crops' are generally purposely bred or selected for human objectivity's (ranging from direct or indirect consumption, feed or industrial applications such as fibers) for example soybean, sunflower, corn, peanut, maize, wheat, cotton, safflower and rapeseed.

The invention provides a method for modulating a developmental pathway of a plant comprising modifying a gene encoding for a gene product or protein belonging to a developmental cascade or signaling complex comprising modifying at least one gene encoding a gene product belonging to the complex of RKS proteins, ELS proteins, NDR/NHL proteins, SBP/SPL proteins and ligand proteins. In one embodiment, the invention provides a method for modulating or modifying organ size. Plant or plant organ size is determined by both cell elongation and cell division rate. Modifying either one or both processes results in a change in final organ size. Increasing the level of specific members of the family of RKS genes results in an increase in organ size, growth rate and yield. Modulating plant growth, organ size and yield of plant organs is the most important process to be optimized in plant performance. Here we show that modulating the level of members of the family of the RKS signaling complex with a method according to the invention is sufficient to modulate these processes. The invention provides herewith a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating

cellular division during plant growth or organ formation, in particular wherein said gene comprises an RKS4 or RKS10 gene or functional equivalent thereof. Inactivation of endogenous RKS gene product results in a decrease in plant growth, proving that the normal function of these endogenous RKS gene products is the regulation of growth and organ size. Use of a method according to invention for elevation of the levels of the regulating of the RKS signaling complex in plant cells is provided in order to increase for example the size of plant organs, the growth rate, the yield of harvested crop, the yield of total plant material or the total plant size. Decreasing the levels of endogenous RKS gene product is provided in order to decrease the size of plant organs, the growth rate, or the total plant size.

In another embodiment, the invention relates to cell division. The mitotic cell cycle in eukaryotes determines the total number of cells within the organism and the number of cells within individual organs. The links between cell proliferation, cell differentiation and cell-cycle machinery are of primary importance for eukaryotes, and regulation of these processes allows modifications during every single stage of development. Here we show that modulating the level of members of the family of the RKS signaling complex is sufficient to modulate these processes. The invention provides herewith a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating cellular division during plant growth or organ formation, in particular wherein said gene comprises an RKS4 or RKS10 gene or functional equivalent Herewith the invention provides a method for modulating the number of cells to be formed within an eukaryotic organism as a whole or for modulating the cell number within individual organs is, which of primary importance in modulating plant developmental processes,

especially of arable plants. Here we show that members of the RKS signaling complex are able to regulate the number of cellular divisions, thereby regulating the total number of cells within the organism or different organs.

In a further embodiment, the invention relates to the regeneration of apical meristem. Modification the levels of different RKS and ELS genes within plants allows the initiation and / or outgrowth of apical meristems, resulting in the formation of large numbers of plantlets from a single source. A number of gene products that is able to increase the regeneration potential of plants is known already. Examples of these are KNAT1, cycD3, CUC2 and IPT. Here we show that modulation of the endogenous levels of RKS genes results in the formation of new shoots and plantlets in different plant species like *Nicotiana tabacum* and *Arabidopsis thaliana*. Herewith the invention provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein, allowing modulating apical meristem formation, in particular wherein said gene comprises an ELS1, RKS0, RKS3, RKS4, RKS8 or RKS10 gene or functional equivalent thereof. A direct application of such a method according to the invention is the stable or transient expression of RKS and ELS genes or gene products in order to initiate vegetative reproduction. Regeneration can be induced after overexpression of for example RKS0 and ELS1; or by co-suppression of for example the endogenous RKS3, RKS4, RKS8 or RKS10 genes. Overexpression or co-suppression of these RKS and ELS gene products can be either transient, or stable by integration of the corresponding expression casettes in the plant genome. A further example of essentially identical functions for for example ELS1 and RKS0 overexpressing plants is for example shown in the detailed description, example 3, where both transgenic constructs are able to induce the

regeneration capacity of in vitro cultured *Arabidopsis* callus. Another example comprises functional interaction between RKS and SBP proteins which was shown by studies in transgenic tobacco plants in which SBP5 and RKS0 were both overexpressed under the control of an enhanced 35S promoter. At the tip of double overexpressing plants, embryostructures appeared whereas in the SBP5 overexpressing plants alone or the RKS0 overexpressing plants alone no phenotype was detectable at the root tips of transgenic tobacco plants. These results show that both RKS and SBP proteins are involved together in a signaling cascade, resulting in the reprogramming of developmental fate of a determined meristem.

Furthermore, it is herein also shown that several RKS genes are able to regulate proper identity and development of meristems and primordia. The invention for example also relates to fasciation, Fasciation is normally a result from an increased size of the apical meristem in apical plant organs. Modulation of the number of cells within the proliferating zone of the shoot apical meristem results in an excess number of cellular divisions, giving rise to excess numbers of primordia formed or to stems in which the number of cells is increased. The invention herewith provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating fasciation, in particular wherein said gene comprises an RKS0, RKS3, RKS8 or RKS10 gene or functional equivalent thereof. Here we for example show that modulation of the levels of RKS gene products in plants like *Arabidopsis thaliana* can result in fasciated stems. A direct application as provided herein is the regulated formation of fasciation in plant species in which such a trait is desired like ornamental plants. Regulation of the initiation and extent of fasciation, either by placing the responsible RKS encoding DNA sequences under the control of stage or tissue specific

promoters, constitutive promoters or inducible promoters results in plants with localized or consitutive fasciation of stem tissue. Another application is modulating the number of primordia by regulation of the process of fasciation. An example is provided by for example sprouts, in which an increased number of primordia will result in an increased numbers of sprouts to be harvested. Fasciation can also result in a strong modification in the structural architecture of the inflorescence, resulting in a terminal group of flowers resembling the *Umbelliferae* type.

Identical phenotypes can be observed when transgenic plants are produced that contain the NHL10 cDNA under control of an enhanced 35S promoter. The resulting phenotype of the resulting flowers show that flower organ primordia are switched in identity, similar as observed for RKS10 and RKS13. These meristematic identity switches are normally never observed in *Arabidopsis* and the fact that two different classes of genes are able to display the same phenotypes in transgenic plants is a clear indication for a process in which both members of the RKS and the NDR/NHL families are involved. The invention also relates to root development. Fasciation is normally a result from an increased size of the apical meristem in apical plant organs. Modulation of the number of cells within the proliferating zone of the root apical meristem results in an excess number of cellular divisions, giving rise to excess numbers of primordia formed or to roots in which the number of cells is increased. Adaptation to soil conditions is possible by regulation of root development of plants. Here we describe several processes in root development that can me manipulated by modification of the levels of RKS signaling complex within the root. The invention provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating root development, in particular

wherein said gene comprises an ELS1, ELS2, RKS1, RKS3, RKS4, RKS6, RKS8 or RKS10 gene or functional equivalent thereof. Root length, a result by either root cells proliferation or elongation, can for example be increased by overexpression of for example RKS3, RKS4, RKS6 and ELS2, or inactivation of the endogenous RKS10 gene product. Root length can also be decreased by decreasing of endogenous RKS1 levels or by strong overexpression of RKS10. The initiation of lateral roots is also regulated by RKS gene products. Overexpression of for example RKS10 can result in a strong increase in the initiation and outgrowth of lateral roots. Co-suppression of RKS1 also resulted in the initiation and outgrowth of large numbers of lateral roots. Root hair formation and elongation is important in determining the total contact surface between plant and soil. A strong increase of root hair length (elongation) can be obtained by overexpression of ELS1 and RKS3 gene products. As the roots of terrestrial plants are involved in the acquisition of water and nutrients, anchorage of the plant, synthesis of plant hormones, interaction with the rhizosphere and storage functions, increasing or decreasing root length, for example for flexible adaptations to different water levels, can be manipulated by overexpressing or cosuppressing RKS and / or ELS gene products. Modulation of the total contact surface between plant cells and the outside environment can be manipulated by regulation lateral root formation (increased by RKS10 overexpression and co-suppression of RKS1). Finally the contact surface between plant cells and the soil can be influenced by modulation of the number of root hairs formed or the elongation of the root hairs, as mediated by ELS1 and RKS3.

In a further embodiment, the invention relates to apical meristem identity. All parts of the plant above the ground are generally the result on one apical shoot meristem that has been initiated early at embryogenesis and that gives rise to all apical organs. This development of a single meristem into complex tissue and repeated patterns is the result of tissue

and stage-dependent differentiation processes within the meristems and its resulting offspring cells. The control of meristem formation, meristem identity and meristem differentiation is therefore an important tool in regulating plant architecture and development. Here we present evidence the function of RKS and ELS gene products in regulation of the meristem identity and the formation and outgrowth of new apical meristems. The invention provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating meristem identity, in particular wherein said gene comprises an ELS1, RKS8, RKS10 or RKS13 gene or functional equivalent thereof. Introduction of for example the RKS10 gene product or an other member of the RKS signaling complex under the control of a tissue and / or stage specific promoter as provided herein allows localized and time regulated increases in the levels of gene product. For example the meristematic identity in a determined meristem might thereby be switched back into an undetermined meristem, thereby changing for example a terminal flower into an undetermined generative meristem.

Another application might be found in changing the meristematic identity at an early time point, during early vegetative growth, thereby switching the vegetative meristem into a generative meristem, allowing early flowering. Modulation of meristem identity in terminal primordia, like for example as shown in Figure 30, where flower organ primordia are converted into terminal flower primordia, allows the formation of completely new types of flowers and fused fruitstructures. Constitutive overexpression of RKS gene products results in plants with many apical meristems, as can clearly been seen in Figure 29, where RKS10 overexpression results in an extremely bushy phenotype.

In another embodiment, the invention relates to male sterility. Male sterility is a highly desired trait in many plant species. For example, manipulation of pollen development is crucial for F1 hybrid seed production, to reduce labour costs and for the production of low-environmental impact genetically engineered crops. In order to produce hybrid seed from inbred plant lines, the male organs are removed from each flower, and pollen from another parent is applied manually to produce the hybrid seed. This labour-intensive method is used with a number of vegetables (e.g. hybrid tomatoes) and with many ornamental plants. Transgenic approaches, in which one or more
introduced gene products interfere with normal pollen initiation and development is therefore highly desired. Especially when the number of revertants (growing normal pollen) is extremely low.
Male sterility in plants is a desired trait that has been shown already in many plant species as a result of the inactivation of expression of a number of genes essential for proper stamen development, mitotic divisions in the pollen stem cells, or male gametogenesis. A method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein, allowing modulating pollen development, in particular wherein said gene comprises an ELS2 or RKS10 gene or functional equivalent thereof.
Here we present data that show that overexpression of gene products, like transmembrane receptor kinases (RKS) and extracellular proteins (ELS) can also result in the formation of male sterility. The ability to induce male sterility by overexpressing specific genes as provided herein allows the opportunity to produce transgenic overexpressing plants in which the pollen development is inhibited. Stable single copy homozygous integration of such overexpressing traits into the

plant genome will render such plants completely sterile, making them excellent material for the production of F1 hybrid seed. Furthermore, the combined integration of a male sterility inducing overexpressing gene coupled directly with another desired transgene result in transgenic plants which are unable to produce transgenic seed, making these transgenic plants excellent material for outside growth without problems affecting transgenic pollen spreading throughout the environment, thereby eliminating possible crosses with wild plant species or other non-transgenic crops. The combination of a desired transgene flanked on both sites by different male-sterility inducing overexpressing genes would decrease the frequency of pollen formation to an extremely low level. An example is an overexpressing construct of RKS10 at the 5'end of integrated DNA fragment, the desired transgene expression cassette in the middle and at the 3'end of the integrated DNA the ELS2 overexpressing construct. This complete DNA fragment is integrated into the genome by conventional techniques, like particle bombardment, *Agrobacterium* transformation etc. Another possible application concerns the modification of pollen in ornamental plant species like lily, where the release of pollen from cut flowers can be avoided by making transgenic plants in which pollen development is initiated by release from the stamen is prevented (a desired trait that can be obtained by overexpressing for example ELS2, resulting in partial pollen development). Hereby the ornamental value of the stamen with pollen is not lost, but release of pollen is inhibited.

Furthermore, surprisingly we observe that NDR NHL gene products share homology with the family of syntaxins, involved in vesicle transport, positioning of cell wall formation and cytokinesis.

Table 1

Homology between members of the syntaxin family and the NDR NHL family

NHL10= At2g35980
maaeqplnga fygpsvpppa pkgyyrrghg rgcgccllsl fvkviisliv ilgvaalifw
livrpraikf hvtdasltrf dhtspdnilr ynlaltvpvr npnkriglyy drieahayye
gkrfstitlt pfyqghkntt vltptfqgqn lvifnagqsr tlnaerisgv ynieikfrlr
vrfklgdlkf rrikpkvdcd dlrlplstsn gttttstvfp ikcdfdf

At1g32270 syntaxin,
MVRSNDVKFQ VYDAELTHFD LESNNNLQYS LSLNLSIRNS KSSIGIHYDR FEATVYYMNQ
RLGAVPMPLF YLGSKNTMLL RALFEGQTLV LLKGNERKKF EDDQKTGVYR IDVKLSINFR
VMVLHLVTWP MKPVVRCHLK IPLALGSSNS TGGHKKMLLI GQLVKDTSAN LREASETDHR
RDVAQSKKIA DAKLAKDFEA ALKEFQKAQH ITVERETSYI PFDPKGSFSS SEVDIGYDRS
QEQRVLMESR RQEIVLLDNE ISLNEARIEA REQGIQEVKH QISEVMEMFK DLAVMVDHQG
TIDDIDEKID NLRSAAAQGK SHLVKASNTQ GSNSSLLFSC SLLLFFFLSG DLCRCVCVGS
ENPRLNPTRR KAWCEEEDEE QRKKQQKKKT MSEKRRREEK KVNKPNGFVF CVLGHK*

Below the homology is shown between NHL10 (Upper line) and a syntaxin protein. (bottom line). The identical amino acids are shown in the middle line.

IVRPRAIKFHVTDASLTRFDHTSPDNILRYNLALTVPVRNPNKRIGLYYDRIEAHAYYEG
 VR KF V DA LT FD S N L Y L L RN IG YDR EA YY
MVRSNDVKFQVYDAELTHFDLESNNN-LQYSLSLNLSIRNSKSSIGIHYDRFEATVYYMN

KRFSTITLTPFYQGHKNTTVLTPTFQGQNLVIFNAGQSRTLNAERISGVYNIEIKFRLRV
 R FY G KNT L F GQ LV GVY I K
QRLGAVPMPLFYLGSKNTMLLRALFEGQTLVLLKGNERKKFEDDQKTGVYRIDVKLSINF

RFKLGDLKFRRIKPKVDCDDLRLPLSTSNGTTT
R L KP V C L PL T
RVMVLHLVTWPMKPVVRCH-LKIPLALGSSNST

That syntaxins and NDR/NHL genes share large homology becomes even more clear when performing a database search using the following site:

http://mips.gsf.de/proj/thal/db/search/search_frame.html

searching for homologous sequences with the sequence At1g32270

gene code:		predicted function:
At1g32270	syntaxin, putative	Syntaxin
At5g46860	syntaxin related protein AtVam3p (gb|AAC49823.1)	Syntaxin
At4g17730	syntaxin	Syntaxin
At5g16830	syntaxin homologue	Syntaxin
At3g11650	unknown protein	Putative syntaxin
At2g35460	similar to harpin-induced protein	Putative syntaxin
At5g06320	harpin-induced protein-like	Putative syntaxin
At2g35980	similar to harpin-induced protein	Putative syntaxin
At1g65690	hypothetical protein	NDR HNL
At4g05220	putative protein	Putative syntaxin
At3g05710	putative syntaxin protein AtSNAP33	Syntaxin
At2g27080	unknown protein	NDR HNL
At3g52470	putative protein	Putative syntaxin
At1g61760	hypothetical protein	Putative syntaxin
At5g21130	putative protein	NDR HNL
At3g52400	syntaxin-like protein synt4	Syntaxin
At2g35960	putative harpin-induced protein	Putative syntaxin
At5g06330	harpin-induced protein-like	Putative syntaxin
At5g26980	tSNARE	Syntaxin
At5g36970	putative protein	Putative syntaxin
At3g44220	putative protein	Putative syntaxin
At3g03800	s-syntaxin-like protein	Syntaxin
At2g35970	putative harpin-induced protein	Putative syntaxin
At4g09590	putative protein	Putative syntaxin
At4g23930	putative protein	
At1g61290	similar to syntaxin-related protein	Syntaxin
At3g11660	unknown protein	Putative syntaxin
At1g54540	hypothetical protein	Putative syntaxin
At3g24350	syntaxin-like protein	Syntaxin
At5g22200	NDR1/HIN1-like	NDR HNL

At1g11250	syntaxin-related protein At-SYR1	Syntaxin
At5g53880		
At3g11820	putative syntaxin	Syntaxin
At3g54200		Putative syntaxin
At5g05760	t-SNARE SED5	Syntaxin
At5g53730		Putative syntaxin
At4g03330	SYR1-like syntaxin 1	Syntaxin
At3g47910		
At5g08080	syntaxin-like protein	Syntaxin
At5g11890		Putative syntaxin
At1g17620		Putative syntaxin
At2g22180		Putative syntaxin
At5g22870		Putative syntaxin
At2g46300		Putative syntaxin
At2g27260		Putative syntaxin
At4g01410		Putative syntaxin
At5g22200		Putative syntaxin
At4g01110		Putative syntaxin
At3g52460		Putative syntaxin
At3g26350		Putative syntaxin
At1g08160		Putative syntaxin
At2g01080		Putative syntaxin
At5g56050		Putative syntaxin
At3g20600		Putative syntaxin
At3g20590		Putative syntaxin
At4g39740		Putative syntaxin
At1g32270		Putative syntaxin
At1g13050		Putative syntaxin
At5g45320		Putative syntaxin
At3g20610		Putative syntaxin
At4g26490		Putative syntaxin
At5942860		Putative syntaxin
At1g45688		Putative syntaxin
At4g26820		Putative syntaxin

This observation provides the explanation for understanding the mechanism by which the RKS / NDR-NHL complex functions. Cell wall immobilized RKS gene products (containing the

extensin-like extracellular domain) respond to a local ligand signal, in combination with the heterodimerizing ELS protein (s) either as homodimers, as RKS heterodimers or in combination with the heterodimerizing ELS protein(s).

Predicted ligands for the RKS / ELS receptor binding consist of peptide ligands (based on the LRR ligand binding domain of this class of receptors). These ligands are normally produced as a pre pro protein. The N-terminal signal sequence is removed by the transport through the Golgi system and allows modification of the ligand at this stage (e.g. glycosylation). The ligands can then be secreted after which further processing is possible (e.c. proteolytic cleavage, removal of sugar groups etc.) The resulting peptide, possible as a monomer or a (hetero)dimerizing molecule binds the transmembrane receptor complex with high affinity, resulting in transmission of the signal from the ligand through the transmembrane receptor component towards the other site of the membrane.

One class of ligands interacting with the RKS and / or ELS receptors consists of the family of pre(pro)proteins shown hereunder in table 3.

Table 3 Ligands within the RKS signaling complex (herein also called RKS/ELS ligand proteins)

For each ligand (A to N) the genomic structure before splicing and processing 5'- towards 3' is given. Exons are indicated in large letters; introns and surrounding sequences (including leader 5'-and trailer sequences 3'-) are indicated in small letters.
Beneath each DNA sequence the amino acid sequence of the pre-pro-peptide is given. The first line represents the signal sequence
The second (set of) lines represents the pro-peptide.
The last line represents the conserved Cysteine motif.

A. At1g22690

```
   1 attaaacgcc aaacactaca tctgtgtttt cgaacaatat tgcgtctgcg tttccttcat
  61 ctatctctct cagtgtcaca atgtctgaac taagagacag ctgtaaacta tcattaagac
 121 ataaactacc aaagtatcaa gctaatgtaa aaattactct catttccacg taacaaattg
 181 agttagctta agatattagt gaaactaggt ttgaattttc ttcttcttct tccatgcatc
 241 ctccgaaaaa agggaaccaa tcaaaactgt ttgcatatca aactccaaca ctttacagca
 301 aatgcaatct ataatctgtg atttatccaa taaaaacctg tgatttatgt ttggctccag
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B. At1g74670

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C. At1g75750

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D. At2g14900

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MKIIVSILVLASLLLISSSLASATIS

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E. At2g18420

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F. At2g30810

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G. At2g39540

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H. At3g02885 (GASA5)

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I. At4g09600 (GASA3)

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 421 tatacttaat tgtagctact aaatagagaa tcagagagaa tagttttata tcttgcacga
 481 aactgcatgc tttttgagac ATGGCAATCT TCCGAAGTAC ACTAGTTTTA CTGCTGATCC
 541 TCTTCTGCCT CACCACTTTT GAGgttcata acttttgtct ttacttctcc atgaatcatt
 601 tgcttcgtct tatccttaat tcatatgtgt ttgatcaatg ataataattc atcattctct
 661 tcagCTTCAT GTTCATGCTG CTGAAGATTC ACAAGTCGGT GAAGGCGTAG TGAAAATTGg
 721 tatgtaacgc taacatatat gtaaagtgtt atatctctgt ttatatatga tttttaaacg
 781 gttaaaaact agtcatatgt gtataaatat atcatgtgaa gATTGCGGTG GGAGATGCAA
 841 AGGTAGATGC AGCAAATCGT CGAGGCCAAA TCTGTGTTTG AGAGCATGCA ACAGCTGTTG
 901 TTACCGCTGC AACTGTGTGC CACCAGGCAC CGCCGGGAAC CACCACCTTT GTCCTTGCTA
 961 CGCCTCCATT ACCACTCGTG GTGGCCGTCT CAAGTGCCCT TAAacatata cacatacaga
1021 tgtgtgtata tgtcttccgc gagcacacac gtacgtttat gttttaagga caatagtatg
1081 tatgagcagc tataaacaaa ccagaagtta atggttcatg ttgaactagt ataagttgta
1141 tgaactgtgc ttcttttgaa caaccacttt tgctgtaagt ttagcaaccc tatttaataa
1201 attagagatt acaaaaaaaa aaatgaaaaa tgtttaaaaa acgtggattt ttaaatttgg
1261 gattaaaaat taattttcat tttggttgat ttgtcaataa attagctaag ttttgtatac
1321 taggccgttt aagatatgct gttaaatttt tgataataga gttgccttag aagttcataa
1381 ctgtaaatat ctaacttcac ttcaatctca caaacacacg aatcaacttc agcactaaga
1441 atcgaattga ccagaactga aagaaagtaa aagaaaagct gaatacagag aatttaacga
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MAIFRSTLVLLLILFCLTTF

ELHVHAAEDSQVGEGVVKID

CGGRCKGRCSKSSRPNLCLRACNSCCYRCNCVPPGTAGNHHLCPCYASITTRGGRLKCP*

J. At4g09610 (GASA2)

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   1 ttaacagttt aacaccataa tgttaaactc ggtttagcat tttggtgtaa ttctacctct
  61 ttaaccatac atactaaaga cgcagagaag ttcatatggt agttaatcgt aaatagctaa
 121 acttttaatt ggggttaaca tattatttaa cacttaacat ttaactattg atctctcatt
 181 tttttttttat taaccaaaat aaattcattt tagaaccaaa cgtttcaaaa actcgtaatg
 241 ttttctcatt aaatcttatc tatagctcac acaaagaaaa actacggaca tgcatgcacc
 301 caattatata catggattat tatttttagt gttataatat gatacaaaat aaaaaacatt
 361 tggatagccg ataggcgata gccactataa atataccaaa gaggttggat tatacatata
 421 gccgtaatac caaagagagt atcagataga aatagttcta atattttgta caactcacag
 481 aaattgcatg agtttcgaac ATGGCAGTCT TCCGAAGTAC ACTGGTTCTG TTACTAATCA
 541 TCGTCTGTCT CACCACTTAT GAGgtttata atatttttgg tctttatagt tccccaagaa
 601 cacctagcaa tattatactc aattcatgtt tatatgataa tgactgatca ttctcttcag
 661 CTTCACGTCC ACGCTGCTGA TGGTGCAAAG GTCGGTGAAG GCGTAGTGAA AATCGgtatg
 721 taaccctaac ttatatataa cacgttggta tataacttaa tatttctgat gggtgcactc
 781 tcttcccaac ttatatatat ctttgttatg gagaatgtct caagctttta atgagatgtt
 841 atatctcgga gaaggaaact atgaactaaa agctttggat tcctttgcaa caaatataaa
 901 cttttgatgg gtttaaacgg attaaattag ttacatgtgt ttgatgaatg tatgtatgat
 961 tgtagATTGT GGTGGGAGAT GCAAAGATAG ATGCAGCAAA TCTTCGAGAA CGAAGCTATG
1021 CTTGAGAGCG TGCAACAGCT GTTGTTCCCG CTGCAACTGT GTGCCACCTG GTACTTCTGG
1081 AAACACCCAC CTTTGTCCTT GCTACGCCTC CATTACCACT CACGGTGGCC GCCTCAAGTG
1141 CCCTTAAaat ttcttctgtg tctgtttctg tttctacttc tatttcgaat atatgtacat
1201 gtgtgtgtac gtgtgtatgt atacaagtac tgctatgttt tggaggacaa aagtatatgt
1261 atgagaagct ataaactaat tagaagttga tggttatgcg tattatcaaa ccgtgttact
1321 tctgaacaac caatttcggt ttgttccaag tttggcaacc ctaaaataaa aattcaaaat
1381 gattggagac tactcgttaa tagacattga aaacgatgaa atctcgttac gtttttatat
1441 tttttgaact gtaatattat tatgcagaag cggttttgta atgggccgac aaaaaaaaag
1501 tggttttgta atggatatga ttcggatcta ttctggaaat ggtctcaaaa agtagagttg
1561 agatctcaat acgaaaatga acccttccgt ttgatttatc aaagcctttt attttgaaaa
1621 cgttaaatcc tcactaggat ctctctt
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MAVFRSTLVLLIIVCLTTY

ELHVHAADGAKVGEGVVKID

CGGRCKDRCSKSSRTKLCLRACNSCCSRCNCVPPGTSGNTHLCPCYASITTHGGRLKCP**

K. At5g15230 (GASA4)

```
      1 aaatattcac cctaaaatga atctaaaaat gtacaaaatc acaggaaaat aaaactaagc
     61 agaaatgtcc taagaaaact aaagttttta aaaaataatc ttcaaagaga tactccaact
    121 ggtgttataa gcaaaacttg atttatcaaa aacaggttca tagtatttta tatttagtac
    181 tataagcttt ccttaaacca tgtgcaaaac catctaccgc agtctaatta ccaatagcaa
    241 gtaataaaat gggactaaca ttggaggcat acgtggaata atataattgg aggaatacag
    301 taataatgat atgtgttgcc acagggaata attgatacga gcaaatgtgt gtatatatag
    361 cttatatgca acatcattgg gtcctcaacc aaaaactcct ctctcagtac acttcttttc
    421 atacctcaag agactaaaac tagtttgagg agatttagag gagtgtttgg ttctttggat
    481 aacaatatcc caaactgaaa ATGGCTAAGT CATATGGAGC TATCTTCCTC TTGACCCTCA
    541 TTGTCCTCTT CATGCTTCAA ACCATGgtaa cacctctatt atttttttct tctttcaatg
    601 tttgaaaata ttgaagataa tatatttgat tgttttcctt attgacgaac gatatgagac
    661 aaatgtgggt tctattattg tacttttagt tggaatatat ttaatttagc ctttttaatg
    721 aaattaattt tacttgtttt tcctctctct ttttttcgtt ttttagGTTA TGGCCTCAAG
    781 TGGATCTAAT GTGAAGTGGA GCCAGgtcag ttttattatt gaatcgacta gtaattacct
    841 tttaaactat attttatacc tattgttatc tcgtaactta acgaaaagtg attaattagt
    901 tacctttttt ggttaatttt cagAAACGTT ATGGACCAGG AAGCCTGAAA CGTACCCgta
    961 agtttttttct tcacagctat tcttaaacaa tttttttta atctcataat cgacgaaaaa
   1021 taaacaattc aagaaatctt ttattgtgtt ataataaaaa aaaataagca tttcagttgc
   1081 agaaaataag ttgaaagtga agtgttaagt ggactgtttg gtcagatccg tagactcaaa
   1141 atatattaga tattgacgaa attgcccctt aatatggtca tacagtcaaa gcaacccact
   1201 atcttgagac ccacaaaaca gtaaaaaaaa aagctaatga atttccacta gattctgttg
   1261 tttttattag taataaaaaa tttttgagtg ttaacatttt gatattgttt gtatttgaaa
   1321 caaccagAAT GCCCATCGGA ATGTGATAGG AGGTGTAAAA AGACACAGTA CCACAAGGCT
   1381 TGCATTACGT TCTGCAACAA ATGCTGCAGG AAGTGTCTCT GTGTGCCTCC GGGTTACTAT
   1441 GGGAACAAAC AAGTTTGCTC CTGCTACAAC AACTGGAAAA CTCAAGAGGG TGGACCAAAA
   1501 TGCCCTTGAa aaaatctccc ttcgttccct ttttataata aaaattttca actataacta
   1561 aatttccttt gatcaatgtt ttatctactt tattcctaat gttgtaatgt tatgtcactc
   1621 cttttcggat tttgttctaa atcctaaaaa aaatgagagt ggccctatga atgatatttt
   1681 tcatgaatac ttgtgtttct aaagatattt tcccattcat ccaccaaaaa aaaagatatt
   1741 ttccatttcg aaaatagtaa tactataaag ggtaaggcaa accaaataat acaatttaaa
   1801 aaattcctgc gaaagaagta tgcatatgta gaaaagagtg acattgggtc tctcggccca
   1861 gtactaaaaa gcccattatt gatttttcca agcttttac aaaatcacgt gttctaacgc
   1921 gattgctttt tgccgcaatc ttcttttata caagacttgg gctttgggca gttggaaata
   1981 aataacgaca acgatatttt acaatcggt
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MAKSYGAIFLLTLIVLFMLQTMV

MASSGSNVKWSQKRYGPGSLKRTQ

CPSECDRRCKKTQYHKACITFCNKCCRKCLCVPPGYYGNKQVCSCYNNWKTQEGGPKCP**

L. At5g14920

```
   1 ttgctcactg gtgcaataat cgaagtgaag agcctcttta tatgaaatat ataagcgaca
  61 cagccttatg ggcaaatcga atgctattta tttatttgat aagaagatta ataatttcaa
 121 tttgtcatcc actagtctct tggggtactc aaaacatatc accaaaaagt ccatagagtt
 181 atttgttctt atttactgat aaagtattcc aagttgatgt acgaataaag tggcaatttc
 241 atgtattatc aatataatcc atttttggga atctgatatt ttgtttatcc tcgagctctg
 301 agagatatat tttggtgcag tgaaggttca aagctggcat gcatgatgca tataataact
 361 gctctggacc taatacttac tacgcattta aattaatatt tatggataat atggttaata
 421 ataaggaac ttctatttat atcacaaaag gtcactggtc ttcttcgtgt gacttcacca
 481 ctttctcatc tcccacaaaa ATGGCTCTCT CACTTCTTTC AGTCTTTATC TTTTTCCATG
 541 TCTTTACCAA Tgtaagttat tcttactttt cataacaaaa ggtgttatta tgttaaagac
 601 tacataatag tatacaatta tgtgcattac gttttcgcgt attgtaacta actatgtatt
 661 ttgattaatc accgagcagG TTGTTTTTGC TGCTTCAAAT GAGGAATCCA ACGCCTTAgt
 721 acgttttcta atttccagtt taattatttc tatgcgtctt taactatata ctcaggcatt
 781 tttattgatt attgtgtatg aagttaaatt ttggtatatg tttgtattaa atttatagGT
 841 TTCTTTACCA ACGCCAACAC TTCCATCGCC ATCTCCGGCT ACCAAACCGC CGTCGCCAGC
 901 TCTCAAACCG CCGACGCCGT CGTACAAGCC ACCCACGCTG CCAACTACTC CTATTAAACC
 961 ACCCACCACA AAACCTCCGG TCAAACCTCC AACTATTCCG GTTACACCAG TAAAACCTCC
1021 GGTTTCAACT CCTCCGATCA AACTACCGCC GGTACAACCA CCTACGTACA AACCCCCAAC
1081 GCCAACAGTT AAACCACCGT CCGTCCAACC ACCTACGTAC AAACCCCCAA CTCCAACGGT
1141 TAAACCACCC ACTACATCAC CGGTTAAACC ACCCACTACG CCACCAGTTC AATCACCGCC
1201 GGTCCAACCA CCTACGTACA AACCCCCAAC GTCACCGGTT AAACCACCCA CCACAACTCC
1261 ACCGGTTAAA CCCCCCACCA CGACGCCACC GGTCCAACCA CCTACGTACA ATCCCCCAAC
1321 TACACCGGTT AAACCACCTA CAGCGCCGCC TGTCAAACCT CCAACACCAC CTCCCGTAAG
1381 AACTCGGATA Ggtaataata attttctttc aaaagtgtga tgattatcgg tcgttgatta
1441 gatcggatgt ataattggac taaattttgg acggtttagA TTGCGTGCCT TTATGTGGGA
1501 CGAGGTGTGG GCAACACTCG AGGAAGAACG TATGTATGAG AGCGTGCGTC ACGTGCTGCT
1561 ACCGCTGCAA GTGTGTTCCC CCAGGCACCT ACGGTAATAA GGAGAAGTGT GGATCTTGTT
1621 ACGCCAACAT GAAGACACGT GGTGGAAAAT CCAAATGTCC TTGAaccttt atatgacgat
1681 ggttgttaaa cgaaataatt taaatcaatg gagtttttat aagtttgtaa tgcgtttgtt
1741 tttgttatag taatattgag ttggatcttt gtttacggga cgtagaatac taaataatga
1801 aaaaaacctt ctcgatgaat taagggtttt atgaatttgt tttgtattga ataatatagg
1861 gatggataaa gttttattat tctaacaggt tactttatta ggcatttctt cggctcatgt
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1981 agaaatgcac atagcgaagc tcaaaagatg agtgttctgc tagcggtaat gttgttattc
2041 agttgggtca aatgctctaa ttgcaaatct tatttgggcc ttatatagac tcttatgtgc
2101 atatggtcca gcctatttgg gccgatgtgt ttgaagatca tttgggaaag tcttgcgcaa
2161 ggag
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MALSLLSVFIFFHVFTNVVFAAS

NEESNALVSLPTPTLPSPSPA
TKPPSPALKPPTPSYKPPTLP
TTPIKPPTTKPPVKPPTIPVT
PVKPPVSTPPIKLPPVQPPTY
KPPTPTVKPPSVQPPTYKPPT
PTVKPPTTSPVKPPTTPPVQS
PPVQPPTYKPPTSPVKPPTTT
PPVKPPTTTPPVQPPTYNPPT
TPVKPPTAPPVKPPTPPPVRT
RID

CVPLCGTRCGQHSRKNVCMRACVTCCYRCKCVPPGTYGNKEKCGSCYANMKTRGGKSKCP*

M. At5g59845

```
   1 gacttgagta tgaatccaat aacccaaaat ttatgcagat tttagaatac ttcttataaa
  61 tcttaaatga ataacacaaa actttaacat acttttaaca aatcttgatt gaataacaac
 121 agattctaca tgacatttta aatcactaaa actcttttga aatcataaac caataacaac
 181 cccttagttt tttactattt gaattctgac gtacttttt attagttgaa tttctataaa
 241 tgagaaaaca ttaattattt cttaatcttt gaacttaagc cccacaaaaa tcttataaat
 301 tgggacagat ggactagata acaagcgttt cacctactcc aaaatttccc tataagtaac
 361 tctttttgta acctcctttt cttcccaaac catcactcct tttgcattgt gtgaaacctt
 421 cgagttttct cttcatcttc tcaaagtaac aaactttctc caaacagatt attattaaaa
 481 caatctcatc aagaactacg ATGAAATTCC CGGCTGTAAA AGTTCTTATT ATCTCTCTTC
 541 TCATCACATC TTCTTTGTTC ATACTCTCAA CCGCGGATTC GTgtaagtat acacaatgca
 601 ttttcttatt ttagatactt ttctcattag aaatttagct ttcttaataa aattgtattg
 661 tgatgatgga ttaattagCA CCATGCGGAG GAAAATGCAA CGTGAGATGT TCAAAGGCAG
 721 GAAGACAAGA TAGGTGTCTC AAGTATTGTA ATATATGTTG CGAGAAGTGT AACTATTGTG
 781 TTCCTTCAGG CACTTATGGA AACAAAGATG AATGCCCTTG TTACCGCGAT ATGAAGAACT
 841 CCAAAGGCAC GTCCAAATGT CCTTGAtcat gttcttaaga ttatccttat agacacaata
 901 tcttgaaatg ttaagattgt gcttgatgcc taaaataatg agcttgagat acttctatga
 961 atgaatatgt gaaagatttt gacaataaaa tgatttgatg tattaaaata ttcttagtga
1021 agttatatat gtataaatga agtatgaaat atacattgta tgttgcttta catgagaaag
1081 ataaatctac aacaatccaa tgtatgaaaa ttttactaag ttaactgatc agaaacgtta
1141 attatggttt agaatcttgt ggagagatga ttacttttgt aagagaaatt gattgtttgt
1201 tgtcaatgag gataaagtaa gaagccattt ctcaacacat ggacttgata gcaaactaaa
1261 caaggctcaa gcattgaaat tgaaacgtct cgatagataa gattggctca agaaaagcaa
1321 gtgtttttg ttgtagaaaa cagaaattga aattactgtc tacttt
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MKFPAVKVLIISLLITSSLFILSTA

DSSP

CGGKCNVRCSKAGRQDRCLKYCNICCEKCNYCVPSGTYGNKDECPCYRDMKNSKGTSKCP*

N. At3g10170

genomic structure before splicing and processing 5'- towards 3'
predicted orf sequences are underlined

CTGTTTTCAGAAAATGGCAACAAAACTTAGCATCATTGTTTTCTCCATTG
TTGTGTTACATCTTCTTCTGTCTGCCCATATGCATGTAAGTGTTTCAACA
CTCTATTCCTCTATGTTCACATTTATCAACTTTATCTTATACGTCCCTGA
ATAAAACACAGCCTATATACTTGGAATCTCCTGCTCGACAACCACAACCA
CCACAGTCGCAACCACAACTGCCGCATCACAATAACTCTCAAGTGAGTTT
CTCGGTTCATCACTACTCAAAAAAAGAGTTTCATCGAATCTACAAAACCT
TTTTAACATCCTTTGCATCTTCTTGTTGATTTTGGCAGTACGGTACTACT
CAAGGCAGTCTTCAACCCCAAGGTAAACCCACTGACTAGCCTAGTTTTTA
ATTAATGTTTGTGCTGAATGCGAAACTAAATCCGCTATTCCACCTTTATT
AGAGTGCGGGCCAAGGTGTGGAGATAGATGCTCGAATACACAATACAAGA
AGCCGTGTTTGTTCTTCTGCAACAAATGTTGTAACAAGTGCTTGTGTGTG
CCCCCAGGTACTTATGGCAATAAGCAAGTATGTCCTTGCTATAACAACTG
GAAGACCAAGAGCGGTGGACCAAAATGCCCTTAGTTTCTCCTCTTAATTA
CTTTAGCATAAACTCCATGTAATTTGTTAATCTACCTATCATAATTTATA
TATGTATTGGACTCTTCCATAATCACATCAGTTCTCTGTGATTATGACGT

Amino acid sequence of the predicted pre-pro-peptide
the first line represents the signal sequence
the second (set of) lines represents the the pro-peptide
the last line represents the conserved Cysteine motif.

MATKLSIIVFSIVVLHLLLSAHMH

FLINVCAECETKSAIPPLLE

CGPRCGDRCSNTQYKKPCLFFCNKCCNKCLCVPPGTYGNKQVCPCYNNWKTKSGGPKCP*

They consist of an N-terminal signal peptide, followed by a variable domain (involved in mobility or cell wall attachment) and a C-terminal domain with 12 conserved cystein residues. The consensus of this last domain is:

C-C-RC--------C---C--CC-(R/K)C-CVP(P/S)GT-G(N/H)---C-CY-------G--KCP*

(-) = any amino acid;

(C) = conserved C-residue

(/) = either one or the other amino acid at this position;

* = stopcodon

Some members of this gene family have been described previously, and represent the GASA family in *Arabidopsis thaliana* (Plant Mol. Biol. 36 (1998). Similar family members containing the same structural motifs are present in rice (like GASR1) and tomato (Plant Journal 2 (1992) 153-159; Mol. Gen. Genet. 243 (1994) Taylor and Scheuring). In *Arabidopsis*, the GASA gene family represents 14 different membres, similar as the number for the RKS gene family. Our data on the similar phenotypes for RKS4 and GASA3 (figure 6) and the fact that there are similar numbers of ligands and receptors suggest that there is a single GASA ligand molecule interaction with a single RKS molecule. T-DNA knock out phenotypes observed with several of the other GASA peptide ligand genes also show modifications of organ and plant size like the appearance of extreme dwarf plants resembling brassinosteroid insensitive mutants. Co-localization of RKS genes and GASA ligands on the genome (see figure 4) could provide clues of molecular interactions between GASA molecules and RKS molecules (similar as for S locus proteins and S locus receptor kinases).

Furthermore, in the chapter discussing the effects of roots in RKS transgenic plants, it was shown that overexpression of RKS genes can result in the formation of lateral roots (figure 26). One of the GASA ligands is involved in the formation and/or outgrowth of lateral roots as discussed in Mol. Gen. Genet. 243, 1994, 148-157.

Intracellularly, this signal is transmitted onto membrane (but not necessarily plasma membrane) associated NDR-NHL proteins. At least some of the functions of the syntaxin-like NDR-NHL proteins would thereby result in the regulation of vesicle transport and /or the positioning of new cell wall formation. Neighboring cells are known to influence and determine the developmental state and the differentiation of cells. In transgenic plants with RKS and / or NDR-NHL expression cassettes the positioning of new cell walls is modified, resulting in abnormal neighboring cells, resulting in abnormal development of groups of cells like flower meristem primordia as observed and shown with RKS0, RKS13 and NHL10.

Table 2 overview of accessions numbers of RKS signal complex genes in *arabidopsis* and in rice:

Gene	code	contig	gene prediction in At database	*Oryza sativa* japonica contig	approximate *position* in bp around:
RKS0	At1g71830	f14o23	ok	OSJNBa0036B21	52.000
RKS1	At1g60800	f8a5	ok	P0038C05	60.000
RKS2	At5g65240	mqn23	ok	OJ1212_C08	8000
RKS3	At5g63710	mbk5	ok	see rks2	
RKS4	At2g23950	t29e15	wrong, exon missing	P0708B04	35.000
RKS5	At5g45780	mra19	wrong, exon missing	OJ1077_A12	102.000
RKS6	At5g10290	wt e 23	ok	see rks2	
RKS7	At5g16000	ku e 24	ok	P0038C05	60.000
RKS8	At1g34210	f23m19	ok	OJ1134_B10	90.000 & 1000 2 different genes!
RKS10	At4g33430	en d 25	wrong, exon missing	see rks0	
RKS11	At4g30520	wu d 20	wrong, exon missing	see rks4	
RKS12	At2g13800	f13j11	wrong, exon missing	see rks10	
RKS13	At2g13790	f13j11	ok	P0633E08	36.000
RKS14	At3g25560	mwl2	wrong, exon missing	OSJNBb0015G09	36.000
ELS1	At5g21090	ch e 52	ok	P0003H10	53.000
ELS2	possibly allelic variant of ELS1 no genomic sequence identified yet				see els1
ELS3	At3g43740	by c 21	ok	P0468B07	52.000

Homology between aa sequences from arabidopsis proteins are compared with the rice databases using:
http://mips.gsf.de/proj/thal/db/search/search_frame.html
protein sequences based on *Oryza sativa* japonica contig sequences.

Arabidopsis thaliana ELS1 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

ttactctcaaattccttttcgatttccctctcttaaacctccgaaagctcac
ATGGCGTCTCGAAACTATCGGTGGGAGCTCTTCGCAGCTTCGTTAACCCTAA
CCTTAGCTTTGATTCACCTGGTCGAAGCAAACTCCGAAGGAGATGCTCTCTA
CGCTCTTCGCCGGAGTTTGACAGATCCAGACCATGTCCTCCAGAGCTGGGAT
CCAACTCTTGTTAATCCTTGTACCTGGTTCCATGTCACCTGTAACCAAGACA
ACCGCGTCACTCGTGTGGATTTGGGAAATTCAAACCTCTCTGGACATCTTGC
GCCTGAGCTTGGGAAGCTTGAACATTTACAGTATCTAGAGCTCTACAAAAAC
AACATCCAAGGAACTATACCTTCCGAACTTGGAAATCTGAAGAATCTCATCA
GCTTGGATCTGTACAACAACAATCTTACAGGGATAGTTCCCACTTCTTTGGG
AAAATTGAAGTCTCTGGTCTTTTTACGGCTTAATGACAACCGATTGACGGTC
CAATCCCTAGAGCACTCACGGCAATCCCAAGCCTTTAAAGTTGTGACGTCTC
AAGCAATGATTTGTGTGGACAATCCCACAAACGGACCCTTTGCTCACATTCC
TTTACAGAACTTTGAGAACAACCCGAGATTGGAGGGACCGGAATTACTCGGT
CTTGCAAGCTACGACACTAACTGCACC<u>TGA</u>acaactggcaaaacctgaaaat
gaagaattgggggtgaccttgtaagaacacttcaccactttatcaaatatc
acatctactatgtaataagtatatatatgtagtccaaaaaaaaaaaaaaaaa

Predicted amino acid sequence of the *Arabidopsis thaliana* ELS1 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt *et al.* (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 4 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich

repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The last domain might be involved in attachment to other proteins or structures within the cell wall.

MASRNYRWELFAASL
TLTLALIHLVEANSEG

DALYALRRSLTDP
DHVLQSWDPTLVN

PCTWFHVTCNQDNRVTRV

DLGNSNLSGHLA
P ELGKLEHLQYLELYKNNIQGTI
PSELGNLKNLISLDLYNNNLTGIV
PTSLGKLKSLVFLRLNDNRLTGPI
PRALTAIPSLKVVDVSSNDLCGTI
PTNGPFAHIPLQNFENNPRLEGPE

LLGLASYDTNCT

Arabidopsis thaliana ELS2 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

aaaattactcaaattcctattagattactctcttcgacctccgatagctcac
ATGGCGTCTCGAAACTATCGGTGGGAGCTCTTCGCAGCTTCGTTAATCCTAA
CCTTAGCTTTGATTCACCTGGTCGAAGCAAACTCCGAAGGAGATGCTCTTTA
CGCTCTTCGCCGGAGTTTAACAGATCCGGACCATGTCCTCCAGAGCTGGGAT
CCAACTCTTGTTAATCCTTGTACCTGGTTCCATGTCACCTGTAACCAAGACA
ACCGCGTCACTCGTGTGGATTTGGGGAATTCAAACCTCTCTGGACATCTTGC
GCCTGAGCTTGGGAAGCTTGAACATTTACAGTATCTAGAGCTCTACAAAAAC
AACATCCAAGGAACTATACCTTCCGAACTTGGAAATCTGAAGAATCTCATCA
GCTTGGATCTGTACAACAACAATCTTACAGGGATAGTTCCCACTTCTTTGGG
AAAATTGAAGTCTCTGGTCTTTTTACGGCTTAATGACAACCGATTGACGGGG
CAATCCCTAGAGCACTCACTGCCAATCCCAAGCCTTAAAAGTTGTGGATGTC
TAAGCAATGATTTGTGTGGAACAATCCCAACAAACGGACCTTTTGCTCACAT
TCCTTTACAGAACTTTGAGAACAACCCGAGGTTGGAGGGACCGGAATTACTC
GGTCTTGCAAGCTACGACACTAACTGCACCTGAagaaattggcaaaacctga
aaatgaagaattgggggggaccttgtaagaacacttcaccactttatcaaat
atcacatctactatgtaataagtatatatatgtagtccaaaaaaaaaatgaa
gaatcgaatagtaatatcatctggtctcaattgagaactttgaggtctgtgt
atgaaaattaaagattgtactgtaatgttcggttgtgggattctgagaagta
acatttgtattggtatggtatcaagttgttctgccttgtctgcaaaaaaaaa

Predicted amino acid sequence of the *Arabidopsis thaliana* ELS2 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt *et al.* (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 4 leucine residues, each separated by seven other amino acids. The third domain

contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The last domain might be involved in attachment to other proteins or structures within the cell wall.

MASRNYRWELFAASL
ILTLALIHLVEANSEG

DALYALRRSLTDP
DHVLQSWDPTLVN

PCTWFHVTCNQDNRVTRV

DLGNSNLSGHLA
P ELGKLEHLQYLQLYKNNIQGTI
PSELGNLKNLISLDLYNNNLTGIV
PTSLGKLKSLVFLRLNDNRLTGPI
PRALTAIPSLKVVDVSSNDLCGTI
PTNGPFAHIPLQNFENNPRLEGPE

LLGLASYDTNCT

Arabidopsis thaliana ELS3 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

ttctctctccggcgaaaaccATGGTGGCGCAAAACAGTCGGCGGGAGCTTCTAGCAGCTT
CCCTGATCCTAACTTTAGCTCTAATTCGTCTAACGGAAGCAAACTCCGAAGGGGACGCTC
TTCACGCGCTTCGCCGGAGCTTATCAGATCCAGACAATGTTGTTCAGAGTTGGGATCCAA
CTCTTGTTAATCCTTGTACTTGGTTTCATGTCACTTGTAATCAACACCATCAAGTCACTC
GTCTGGATTTGGGGAATTCAAACTTATCTGGACATCTAGTACCTGAACTTGGGAAGCTTG
AACATTTACAATATCTTGAACTCTACAAAAACGAGATTCAAGGAACTATACCTTCTGAGC
TTGGAAATCTGAAGAGTCTAATCAGTTTGGATCTGTACAACAACAATCTCACCGGGAAAA
TCCCATCTTCTTTGGGAAAATTGAAGCGGCTTAACGAAAACCGATTGACCGGTCCTATTC
CTAGAGAACTCACAGTTATTTCAAGCCTTAAAGTTGTTGATGTCTCAGGGAATGATTTGT
GTGGAACAATTCCAGTAGAAGGACCTTTTGAACACATTCCTATGCAAAACTTTGAGAACA
ACCTGAGATTGGAGGGACCAGAACTACTAGGTCTTGCGAGCTATGACACCAATTGCACTT
AAaaagaagttgaagaa

Predicted amino acid sequence of the *Arabidopsis thaliana* ELS3 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt *et al.* (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 2 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The last domain might be involved in attachment to other proteins or structures within the cell wall.

MVAQNSRRELLAASL

ILTLALIRLTEANSEG

DALHALRRSLSDP

DNVVQSWDPTLVN

PCTWFHVTCNQHHQVTRL

DLGNSNLSGHLV

P ELGKLEHLQYLELYKNEIQGTI

PSELGNLKSLISLDLYNNNLTGKI

P SSLGKLKRLNENRLTGPI

PRELTVISSLKVVDVSGNDLCGTI

PVEGPFEHIPMQNFENNLRLEGPE

LLGLASYDTNCT

Arabidopsis thaliana RKS0 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

attttattttatttttactctttgtttgttttaatgctaatgggtttttaaaagggtt
atcgaaaaaatgagtgagtttgtgttgaggttgtctctgtaaagtgttaatggtggtgat
tttcggaagttagggttttctcggatctgaagagatcaaatcaagattcgaaatttacca
ttgttgtttgaa**ATG**GAGTCGAGTTATGTGGTGTTTATCTTACTTTCACTGATCTTACTT
CCGAATCATTCACTGTGGCTTGCTTCTGCTAATTTGGAAGGTGATGCTTTGCATACTTTG
AGGGTTACTCTAGTTGATCCAAACAATGTCTTGCAGAGCTGGGATCCTACGCTAGTGAAT
CCTTGCACATGGTTCCATGTCACTTGCAACAACGAGAACAGTGTCATAAGAGTTGATTTG
GGGAATGCAGAGTTATCTGGCCATTTAGTTCCAGAGCTTGGTGTGCTCAAGAATTTGCAG
TATTTGGAGCTTTACAGTAACAACATAACTGGCCCGATTCCTAGTAATCTTGGAAATCTG
ACAAACTTAGTGAGTTTGGATCTTTACTTAAACAGCTTCTCCGGTCCTATTCCGGAATCA
TTGGGAAAGCTTTCAAAGCTGAGATTTCTCCGGCTTAACAACAACAGTCTCACTGGGTCA
ATTCCTATGTCACTGACCAATATTACTACCCTTCAAGTGTTAGATCTATCAAATAACAGA
CTCTCTGGTTCAGTTCCTGACAATGGCTCCTTCTCACTCTTCACACCCATCAGTTTTGCT
AATAACTTAGACCTATGTGGACCTGTTACAAGTCACCCATGTCCTGGATCTCCCCCGTTT
TCTCCTCCACCACCTTTTATTCAACCTCCCCCAGTTTCCACCCCGAGTGGGTATGGTATA
ACTGGAGCAATAGCTGGTGGAGTTGCTGCAGGTGCTGCTTTGCCCTTTGCTGCTCCTGCA
ATAGCCTTTGCTTGGTGGCGACGAAGAAGCCCACTAGATATTTTCTTCGATGTCCCTGCC
GAAGAAGATCCAGAAGTTCATCTGGGACAGCTCAAGAGGTTTTCTTTGCGGGAGCTACAA
GTGGCGAGTGATGGGTTTAGTAACAAGAACATTTTGGGCAGAGGTGGGTTTGGGAAAGTC
TACAAGGGACGCTTGGCAGACGGAACTCTTGTTGCTGTCAAGAGACTGAAGGAAGAGCGA
ACTCCAGGTGGAGAGCTCCAGTTTCAAACAGAAGTAGAGATGATAAGTATGGCAGTTCAT
CGAAACCTGTTGAGATTACGAGGTTTCTGTATGACACCGACCGAGAGATTGCTTGTGTAT
CCTTACATGGCCAATGGAAGTGTTGCTTCGTGTCTCAGAGAGAGGCCACCGTCACAACCT
CCGCTTGATTGGCCAACGCGGAAGAGAATCGCGCTAGGCTCAGCTCGAGGTTTGTCTTAC
CTACATGATCACTGCGATCCGAAGATCATTCACCGTGACGTAAAAGCAGCAAACATCCTC
TTAGACGAAGAATTCGAAGCGGTTGTTGGAGATTTCGGGTTGGCAAAGCTTATGGACTAT
AAAGACACTCACGTGACAACAGCAGTCCGTGGCACCATCGGTCACATCGCTCCAGAATAT
CTCTCAACCGGAAAATCTTCAGAGAAAACCGACGTTTTCGGATACGGAATCATGCTTCTA
GAACTAATCACAGGACAAAGAGCTTTCGATCTCGCTCGGCTAGCTAACGACGACGACGTC
ATGTTACTTGACTGGGTGAAAGGATTGTTGAAGGAGAAGAAGCTAGAGATGTTAGTGGAT
CCAGATCTTCAAACAAACTACGAGGAGAGAGAACTGGAACAAGTGATACAAGTGGCGTTG

CTATGCACGCAAGGATCACCAATGGAAAGACCAAAGATGTCTGAAGTTGTAAGGATGCTG
GAAGGAGATGGGCTTGCGGAGAAATGGGACGAATGGCAAAAAGTTGAGATTTTGAGGGAA
GAGATTGATTTGAGTCCTAATCCTAACTCTGATTGGATTCTTGATTCTACTTACAATTTG
CACGCCGTTGAGTTATCTGGTCCAAGGTAAaaaaaaaaaaaaaaaa

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS0 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt *et al.* (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 4 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eight domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

MESSYVVFILLSLILLPNHSL
WLASANLEG

DALHTLRVTLVDP
NNVLQSWDPTLVN

PCTWFHVTCNNENSVIRV

DLGNAELSGHLV
P ELGVLKNLQYLELYSNNITGPI

PSNLGNLTNLVSLDLYLNSFSGPI
PESLGKLSKLRFLRLNNNSLTGSI
PMSLTNITTLQVLDLSNNRLSGSV
PDNGSFSLFTPISFANNLDLCGPV

TSHPCPGSPPFSPPPP
FIQPPPVSTPSGYGITG

AIAGGVAAGAAL
PFAAPAIAFAWW

RRRKPLDIFFDVPAEEDPE
VHLGQLKRFSLRELQVAS

DGFSNKNILGRGGFGKVYKGRLAD
GTLVAVKRLKEERTPGGELQFQ
TEVEMISMAVHRNLLRLRGFCM
TPTERLLVYPYMANGSVASCLR
ERPPSQPPLDWPTRKRIALGSA
RGLSYLHDHCDPKIIHRDVKAA
NILLDEEFEAVVGDFGLAKLMD
YKDTHVTTAVRGTIGHIAPEYL
STGKSSEKTDVFGYGIMLLELI
TGQRAFDLARLANDDDVMLLDW
VKGLLKEKKLEMLVDPDLQTNY
EERELEQVIQVALLCTQGSPME
RPKMSEVVRMLE

GDGLAEKWDEWQKVEILREEIDLS

PNPNSDWILDSTYNLHAVELSGPR

Arabidopsis thaliana RKS1 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

ccaaagttgattgctttaagaagggat**ATG**GAAGGTGTGAGATTTGTGGTGTGGAGATTA
GGATTTCTGGTTTTTGTATGGTTCTTTGATATCTCTTCTGCTACACTTTCTCCTACTGGT
GTAAACTATGAAGTGACAGCTTTGGTTGCTGTGAAGAATGAATTGAATGATCCGTACAAA
GTTCTTGAGAATTGGGATGTGAATTCAGTTGATCCTTGTAGCTGGAGAATGGTTTCTTGC
ACTGATGGCTATGTCTCTTCACTGGATCTTCCTAGCCAAAGCTTGTCTGGTACATTGTCT
CCTAGAATCGGAAACCTCACCTATTTACAATCAGTGGTGTTGCAAAACAATGCAATCACT
GGTCCAATTCCGGAAACGATTGGGAGGTTGGAGAAGCTTCAGTCACTTGATCTTTCGAAC
AATTCATTCACCGGGGAGATACCGGCCTCACTTGGAGAACTCAAGAACTTGAATTACTTG
CGGTTAAACAATAACAGTCTTATAGGAACTTGCCCTGAGTCTCTATCCAAGATTGAGGGA
CTCACTCTAGTCGACATTTCGTATAACAATCTTAGTGGTTCGCTGCCAAAAGTTTCTGCC
AGAACTTTCAAGGTAATTGGTAATGCGTTAATCTGTGGCCCAAAAGCTGTTTCAAACTGT
TCTGCTGTTCCCGAGCCTCTCACGCTTCCACAAGATGGTCCAGATGAATCAGGAACTCGT
ACCAATGGCCATCACGTTGCTCTTGCATTTGCCGCAAGCTTCAGTGCAGCATTTTTTGTT
TTCTTTACAAGCGGAATGTTTCTTTGGTGGAGATATCGCCGTAACAAGCAAATATTTTTT
GACGTTAATGAACAATATGATCCAGAAGTGAGTTTAGGGCACTTGAAGAGGTATACATTC
AAAGAGCTTAGATCTGCCACCAATCATTTCAACTCGAAGAACATTCTCGGAAGAGGCGGA
TACGGGATTGTGTACAAAGGACACTTAAACGATGGAACTTTGGTGGCTGTCAAACGTCTC
AAGGACTGTAACATTGCGGGTGGAGAAGTCCAGTTTCAGACAGAAGTAGAGACTATAAGT
TTGGCTCTTCATCGCAATCTCCTCCGGCTCCGCGGTTTCTGTAGTAGCAACCAGGAGAGA
ATTTTAGTCTACCCTTACATGCCAAATGGGAGTGTCGCATCACGCTTAAAAGATAATATC
CGTGGAGAGCCAGCATTAGACTGGTCGAGAAGGAAGAAGATAGCGGTTGGGACAGCGAGA
GGACTAGTTTACCTACACGAGCAATGTGACCCGAAGATTATACACCGCGATGTGAAAGCA
GCTAACATTCTGTTAGATGAGGACTTCGAAGCAGTTGTTGGTGATTTTGGGTTAGCTAAG
CTTCTAGACCATAGAGACTCTCATGTCACAACTGCAGTCCGTGGAACTGTTGGCCACATT
GCACCTGAGTACTTATCCACGGGTCAGTCCTCAGAGAAGACTGATGTCTTTGGCTTTGGC
ATACTTCTCCTTGAGCTCATTACTGGTCAGAAAGCTCTTGATTTTGGCAGATCCGCACAC
CAGAAAGGTGTAATGCTTGACTGGGTGAAGAAGCTGCACCAAGAAGGGAAACTAAAGCAG
TTAATAGACAAAGATCTAAATGACAAGTTCGATAGAGTAGAACTCGAAGAAATCGTTCAA
GTTGCGCTACTCTGCACTCAATTCAATCCATCTCATCGACCGAAAATGTCAGAAGTTATG
AAGATGCTTGAAGGTGACGGTTTGGCTGAGAGATGGGAAGCGACGCAGAACGGTACTGGT
GAGCATCAGCCACCGCCATTGCCACCGGGGATGGTGAGTTCTTCGCCGCGTGTGAGGTAT

TACTCGGATTATATTCAGGAATCGTCTCTTGTAGTAGAAGCCATTGAGCTCTCGGGTCCT
CGATGAttatgactcactgtttttaaaaaa

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS1 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 3 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eight domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

MEGVRFVVWRLGFL
VFVWFFDISSATLSPTGVNYEV

TALVAVKNELNDP
YKVLENWDVNSVD

PCSWRMVSCTDGYVSSL

DLPSQSLSGT
LSPRIGNLTYLQSVLQNNAITGPI
PETIGRLEKLQSLDLSNNSFTGEI
PASLGELKNLNYLRLNNNSLIGTC
PESLSKIEGLTLVDISYNNLSGSL
PKVSARTFK VIGNALICGPK

AVSNCSAVPEPLTL
PQDGPDESGTRTNG

HHVALAFAASFS
AAFFVFFTSGMFLWW

RYRRNKQIFFDVNEQYDPE
VSLGHLKRYTFKELRSAT

NHFNSKNILGRGGYGIVYKGHLND
GTLVAVKRLKDCNIAGGEVQFQ
TEVETISLALHRNLLRLRGFCS
SNQERILVYPYMPNGSVASRLK
DNIRGEPALDWSRRKKIAVGTA
RGLVYLHEQCDPKIIHRDVKAA
NILLDEDFEAVVGDFGLAKLLD
HRDSHVTTAVRGTVGHIAPEYL
STGQSSEKTDVFGFGILLLELI
TGQKALDFGRSAHQKGVMLDW
VKKLHQEGKLKQLIDKDLNDKF
DRVELEEIVQVALLCTQFNPSH
RPKMSEVMKMLE

GDGLAERWEATQNGTGEHQPPPLPPGMVSSS

PRVRYYSDYIQESSLVVEAIELSGPR

Arabidopsis thaliana RKS2 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

Italics indicate the presence of an alternatively spliced gene product.

tcaattttggtagctcttagaaaa**ATG**GCTCTGCTTATTATCACTGCCTTAGTTTTTAGT
AGTTTATGGTCATCTGTGTCACCAGATGCTCAAGGGGATGCATTATTTGCGTTGAGGAGC
TCGTTACGTGCATCTCCTGAACAGCTTAGTGATTGGAACCAGAATCAAGTCGATCCTTGT
ACTTGGTCTCAAGTTATTTGTGATGACAAGAAACATGTTACTTCTGTAACCTTGTCTTAC
ATGAACTTCTCCTCGGGAACACTGTCTTCAGGAATAGGAATCTTGACAACTCTCAAGACT
CTTACATTGAAGGGAAATGGAATAATGGGTGGAATACCAGAATCCATTGGAAATCTGTCT
AGCTTGACCAGCTTAGATTTGGAGGATAATCACTTAACTGATCGCATTCCATCCACTCTC
GGTAATCTCAAGAATCTACAGTTCTTCAGGACCTTGAGTAGGAATAACCTTAATGGTTCT
ATCCCGGATTCACTTACAGGTCTATCAAAACTGATAAATATTCTGCTCGACTCAAATAAT
CTCAGTGG*GTGAGATTCCTCAGAGTTTATTCAAAATCCCAAAATACAATT*TCACAGCAAAC
AACTTGAGCTGTGGTGGCACTTTCCCGCAACCTTGTGTAACCGAGTCCAGTCCTTCAGGT
GATTCAAGCAGTAGAAAAACTGGAATCATCGCTGGAGTTGTTAGCGGAATAGCGGTTATT
CTACTAGGATTCTTCTTCTTTTTCTTCTGCAAGGATAAACATAAAGGATATAAACGAGAC
GTATTTGTGGATGTTGCAGGAACGAACTTTAAAAAAGGTTTGATTTCAGGTGAAGTGGAC
AGAAGGATTGCTTTTGGACAGTTGAGAAGATTTGCATGGAGAGAGCTTCAGTTGGCTACA
GATGAGTTCAGTGAAAAGAATGTTCTCGGACAAGGAGGCTTTGGGAAAGTTTACAAAGGA
TTGCTTTCGGATGGCACCAAAGTCGCTGTAAAAAGATTGACTGATTTTGAACGTCCAGGA
GGAGATGAAGCTTTCCAGAGAGAAGTTGAGATGATAAGTGTAGCTGTTCATAGGAATCTG
CTTCGCCTTATCGGCTTTTGTACAACACAAACTGAACGACTTTTGGTGTATCCTTTCATG
CAGAATCTAAGTGTTGCATATTGCTTAAGAGAGATTAAACCCGGGGATCCAGTTCTGGAT
TGGTTCAGGAGGAAACAGATTGCGTTAGGTGCAGCACGAGGACTCGAATATCTTCATGAA
CATTGCAACCCGAAGATCATACACAGAGATGTGAAAGCTGCAAATGTGTTACTAGATGAA
GACTTTGAAGCAGTGGTTGGTGATTTTGGTTTAGCCAAGTTGGTAGATGTTAGAAGGACT
AATGTAACCACTCAGGTCCGAGGAACAATGGGTCATATTGCACCAGAATGTATATCCACA
GGGAAATCGTCAGAGAAAACCGATGTTTTCGGGTACGGAATTATGCTTCTGGAGCTTGTA
ACTGGACAAAGAGCAATTGATTTCTCGCGGTTAGAGGAAGAAGATGATGTCTTATTGCTA
GACCATGTGAAGAAACTGGAAAGAGAGAAGAGATTAGAAGACATAGTAGATAAGAAGCTT
GATGAGGATTATATAAAGGAAGAAGTTGAAATGATGATACAAGTAGCTCTGCTATGCACA
CAAGCAGCACCGGAAGAACGACCAGCGATGTCGGAAGTAGTAAGAATGCTAGAAGGAGAA
GGGCTTGCAGAGAGATGGGAAGAGTGGCAGAATCTTGAAGTGACGAGACAAGAAGAGTTT

CAGAGGTTGCAGAGGAGATTTGATTGGGGTGAAGATTCCATTAATAATCAAGATGCTATT
GAATTATCTGGTGGAAGATAGaaacaaaaaa

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS2 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 3 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 3 complete and 2 incomplete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eight domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions. Italics indicate an alternatively spliced gene product.

MALLIITALVFSSL
WSSVSPDAQG

DALFALRSSLR
ASPEQLSDWNQNQVD

PCTWSQVICDDKKHVTSV

TLSYMNFSS GTLSSGI
G ILTTLKTLTLKGNGIMGGI
PESIGNLSSLTSLDLEDNHLTDRI
PSTLGNLKNLQFLTLSRNNLNGSI
PDSLTGLSKLINILLDSNNLS*GEI*
PQSLFKIPKYN FTANNLSCGG

TFPQPCVTESSPSGDSSSRKTG

IIAGVVSGIAVIL
LGFFFFFFC

KDKHKGYKRDVFVDVAGTNFKKGLISGE
VDRRIAFGQLRRFAWRELQLAT

DEFSEKNVLGQGGFGKVYKGLLSD
GTKVAVKRLTDFERPGGDEAFQ
REVEMISVAVHRNLLRLIGFCT
TQTERLLVYPFMQNLSVAYCLR
EIKPGDPVLDWFRRKQIALGAA
RGLEYLHEHCNPKIIHRDVKAA
NVLLDEDFEAVVGDFGLAKLVD
VRRTNVTTQVRGTMGHIAPECI
STGKSSEKTDVFGYGIMLLELV
TGQRAIDFSRLEEEDDVLLLDH
VKKLEREKRLEDIVDKKLDEDY
IKEEVEMMIQVALLCTQAAPEE
RPAMSEVVRMLE

GEGLAERWEEWQNLEVTRQEEFQ

RLQRRFDWGEDSINNQDAIELSGGR

Arabidopsis thaliana RKS3 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

aacggtgaaagtttccatgatcctcttcgaggattcattcaaagaaattgctttagatgg
aacaatcagaaattgatcttacaatgtttc**ATG**GCCTTAGCTTTTGTGGGAATCACTTCG
TCAACAACTCAACCAGATATCGAAGGAGGAGCTCTGTTGCAGCTCAGAGATTCGCTTAAT
GATTCGAGCAATCGTCTAAAATGGACACGCGATTTTGTGAGCCCTTGCTATAGTTGGTCT
TATGTTACCTGCAGAGGCCAGAGTGTTGTGGCTCTAAATCTTGCCTCGAGTGGATTCACA
GGAACACTCTCTCCAGCTATTACAAAACTGAAGTTCTTGGTTACCTTAGAGTTACAGAAC
AATAGTTTATCTGGTGCCTTACCAGATTCTCTTGGGAACATGGTTAATCTACAGACTTTA
AACCTATCAGTGAATAGTTTCAGCGGATCGATACCAGCGAGCTGGAGTCAGCTCTCGAAT
CTAAAGCACTTGGATCTCTCATCCAATAATTTAACAGGAAGCATCCCAACACAATTCTTC
TCAATCCCAACATTCGATTTTTCAGGAACTCAGCTTATATGCGGTAAAAGTTTGAATCAG
CCTTGTTCTTCAAGTTCTCGTCTTCCAGTCACATCCTCCAAGAAAAAGCTGAGAGACATT
ACTTTGACTGCAAGTTGTGTTGCTTCTATAATCTTATTCCTTGGAGCAATGGTTATGTAT
CATCACCATCGCGTCCGCAGAACCAAATACGACATCTTTTTTGATGTAGCTGGGGAAGAT
GACAGGAAGATTTCCTTTGGACAACTAAAACGATTCTCTTTACGTGAAATCCAGCTCGCA
ACAGATAGTTTCAACGAGAGCAATTTGATAGGACAAGGAGGATTTGGTAAAGTATACAGA
GGTTTGCTTCCAGACAAAACAAAAGTTGCAGTGAAACGCCTTGCGGATTACTTCAGTCCT
GGAGGAGAAGCTGCTTTCCAAAGAGAGATTCAGCTCATAAGCGTTGCGGTTCATAAAAAT
CTCTTACGCCTTATTGGCTTCTGCACAACTTCCTCTGAGAGAATCCTTGTTTATCCATAC
ATGGAAAATCTTAGTGTTGCATATCGACTAAGAGATTTGAAAGCGGGAGAGGAAGGATTA
GACTGGCCAACAAGGAAGCGTGTAGCTTTTGGTTCAGCTCACGGTTTAGAGTATCTACAC
GAACATTGTAACCCGAAGATCATACACCGCGATCTCAAGGCTGCAAACATACTTTTAGAC
AACAATTTTGAGCCAGTTCTTGGAGATTTCGGTTTAGCTAAGCTTGTGGACACATCTCTG
ACTCATGTCACAACTCAAGTCCGAGGCACAATGGGTCACATTGCGCCAGAGTATCTCTGC
ACAGGAAAATCATCTGAAAAAACCGATGTTTTTGGTTACGGTATAACGCTTCTTGAGCTT
GTTACTGGTCAGCGCGCAATCGATTTTTCACGCTTGGAAGAAGAGGAAAATATTCTCTTG
CTTGATCATATAAAGAAGTTGCTTAGAGAACAGAGACTTAGAGACATTGTTGATAGCAAT
TTGACTACATATGACTCCAAAGAAGTTGAAACAATCGTTCAAGTGGCTCTTCTCTGCACA
CAAGGCTCACCAGAAGATAGACCAGCGATGTCTGAAGTGGTCAAAATGCTTCAAGGGACT
GGTGGTTTGGCTGAGAAATGGACTGAATGGGAACAACTTGAAGAAGTTAGGAACAAAGAA
GCATTGTTGCTTCCGACTTTACCGGCTACTTGGGATGAAGAAGAAACCACCGTTGATCAA
GAATCTATCCGATTATCGACAGCAAGA**TGA**agaagaaacagagagagaaagatatctatg
aaaa

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS3 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 3 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 4 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eight domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

MALAFVGITSSTTQPDIEG

GALLQLRDSLNDSSNRL
KWTRDFVS

PCYSWSYVTCRGQSVVAL

NLASSGFTGTLS
P AITKLKFLVTLELQNNSLSGAL
PDSLGNMVNLQTLNLSVNSFSGSI

PASWSQLSNLKHLDLSSNNLTGSI
PTQFFSIPTFEFSGTQLICGKS

LNQPCSSSRLPVTSSKKKLRD

ITLTASCVASIIL
FLGAMVMYHHH

RVRRTKYDIFFDVAGEDDR
KISFGQLKRFSLREIQLAT

DSFNESNLIGQGGFGKVYRGLLPD
KTKVAVKRLADYFSPGGEAAFQ
REIQLISVAVHKNLLRLIGFCT
TSSERILVYPYMENLSVAYRLR
DLKAGEEGLDWPTRKRVAFGSA
HGLEYLHEHCNPKIIHRDLKAA
NILLDNNFEPVLGDFGLAKLVD
TSLTHVTTQVRGTMGHIAPEYL
CTGKSSEKTDVFGYGITLLELV
TGQRAIDFSRLEEEENILLLD
HIKKLLREQRLRDIVDSNLTTY
DSKEVETIVQVALLCTQGSPED
RPAMSEVVKMLQ

GTGGLAEKWTEWEQLEEVRNKEALLL

PTLPATWDEEETTVDQESIRLSTAR

Arabidopsis thaliana RKS4 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

tcttccttctccttctggtaatctaatctaaagcttttcATGGTGGTGATGAAGATATTC
TCTGTTCTGTTACTACTATGTTTCTTCGTTACTTGTTCTCTCTCTTCTGAACCCAGAAAC
CCTGAAGTGGAGGCGTTGATAAACATAAAGAACGAGTTACATGATCCACATGGTGTTTTC
AAAAACTGGGATGAGTTTTCTGTTGATCCTTGTAGCTGGACTATGATCTCTTGTTCTTCA
GACAACCTCGTAATTGGCTTAGGAGCTCCAAGTCAGTCTCTTTCAGGAACTTTATCTGGG
TCTATTGGAAATCTCACTAATCTTCGACAAGTGTCATTACAGAACAATAACATCTCCGGT
AAAATCCCACCGGAGATTTGTTCTCTTCCCAAATTACAGACTCTGGATTTATCCAATAAC
CGGTTCTCCGGTGAAATCCCCGGTTCTGTTAACCAGCTGAGTAATCTCCAATATCTGTTG
AACAACAACTCATTATCTGGGCCCTTTCCTGCTTCTCTGTCTCAAATCCCTCACCTCTCT
TTCTTAGACTTGTCTTATAACAATCTCAGAGGTCCTGTTCCTAAATTTCCTGCAAGGACA
TTCAATGTTGCTGGGAACCCTTTGATTTGTAAAAACAGCCTACCGGAGATTTGTTCAGGA
TCAATCAGTGCAAGCCCTCTTTCTGTCTCTTTACGTTCTTCATCAGGACGTAGAACCAAC
ATATTAGCAGTTGCACTTGGTGTAAGCCTTGGCTTTGCTGTTAGTGTAATCCTCTCTCTC
GGGTTCATTTGGTATCGAAAGAAACAAAGACGGTTAACGATGCTTCGCATTAACAAGCAA
GAGGAAGGGTTACTTGGGTTGGGAAATCTAAGAAGCTTCACATTCAGGGAACTTCATGTA
GCTACGGATGGTTTTAGTTCCAAGAGTATTCTTGGTGCTGGTGGGTTTGGTAATGTCTAC
AGAGGAAAATTCGGGGATGGGACAGTGGTTGCAGTGAAACGATTGAAAGATGTGAATGGA
ACCTCCGGGAACTCACAGTTTCGTACTGAGCTTGAGATGATCAGCTTAGCTGTTCATAGG
AATTTGCTTCGGTTAATCGGTTATTGTGCGAGTTCTAGCGAAAGACTTCTTGTTTACCCT
TACATGTCCAATGGCAGCGTCGCCTCTAGGCTCAAAGCTAAGCCAGCGTTGGACTGGAAC
ACAAGGAAGAAGATAGCGATTGGAGCTGCAAGAGGGTTGTTTTATCTACACGAGCAATGC
GATCCCAAGATTATTCACCGAGATGTCAAGGCAGCAAACATTCTCCTAGATGAGTATTTT
GAAGCAGTTGTTGGGGATTTTGGACTAGCAAAGCTACTCAACCACGAGGATTCACATGTC
ACAACCGCGGTTAGAGGAACTGTTGGTCACATTGCACCTGAGTATCTCTCCACCGGTCAG
TCATCTGAGAAAACCGATGTCTTTGGGTTCGGTATACTTTTGCTAGAGCTCATCACAGGA
ATGAGAGCTCTCGAGTTTGGCAAGTCTGTTAGCCAGAAAGGAGCTATGCTAGAATGGGTG
AGGAAGCTACACAAGGAAATGAAAGTAGAGGAGCTAGTAGACCGAGAACTGGGGACAACC
TACGATAGAATAGAAGTTGGAGAGATGCTACAAGTGGCACTGCTCTGCACTCAGTTTCTT
CCAGCTCACAGACCCAAAATGTCTGAAGTAGTTCAGATGCTTGAAGGAGATGGATTAGCT
GAGAGATGGGCTGCTTCACATGACCATTCACATTTCTACCATGCCAACATGTCTTACAGG
ACTATTACCTCTACTGATGGCAACAACCAAACCAAACATCTGTTTGGCTCCTCAGGATTT

GAAGATGAAGATGATAATCAAGCGTTAGATTCATTCGCCATGGAACTATCTGGTCCAAGG
TAGtaaatcttggacacagaaagaaacagatataatatccccatgacttcaatttttgtt

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS4 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 2 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eight domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

MVVMKLITMKIFSVLLLL
CFFVTCSLSSEPRNPEV

EALINIKNELHDP
HGVFKNWDEFSVD

PCSWTMISCSSDNLVIGL

GAPSQSLSGTLS

G SIGNLTNLRQVSLQNNNISGKI

PPEICSLPKLQTLDLSNNRFSGEI

PGSVNQLSNLQYLRLNNNSLSGPF

PASLSQIPHLSFLDLSYNNLRGPV

PKFPARTFNVAGNPLICKNS

LPEICSGSISASPL

SVSLRSSSGRRTN

ILAVALGVSLGFAVSVIL

SLGFIWY

RKKQRRLTMLRINKQEE

GLLGLGNLRSFTFRELHVAT

DGFSSKSILGAGGFGNVYRGKFGD

GTVVAVKRLKDVNGTSGNSQFR

TELEMISLAVHRNLLRLIGYCA

SSSERLLVYPYMSNGSVASRLK

AKPALDWNTRKKIAIGAA

RGLFYLHEQCDPKIIHRDVKAA

NILLDEYFEAVVGDFGLAKLLN

HEDSHVTTAVRGTVGHIAPEYL

STGQSSEKTDVFGFGILLLELI

TGMRALEFGKSVSQKGAMLEW

VRKLHKEMKVEELVDRELGTTY

DRIEVGEMLQVALLCTQFLPAH

RPKMSEVVQMLE

GDGLAERWAASHDHSHFYHANM

SYRTITSTDGNNQTKHLFG

SSGFEDEDDNQALDSFAMELSGPR

Arabidopsis thaliana RKS5 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

ctagagaattcttatacttttctacg**ATG**GAGATTTCTTTGATGAAGTTTCTGTTTTTA
GGAATCTGGGTTTATTATTACTCTGTTCTTGACTCTGTTTCTGCCATGGATAGTCTTTTA
TCTCCCAAGGTGGCTGCGTTAATGTCAGTGAAGAACAAGATGAAAGATGAGAAAGAGGTT
TTGTCTGGTTGGGATATTAACTCTGTTGATCCTTGTACTTGGAACATGGTTGGTTGTTCT
TCTGAAGGTTTTGTGGTTTCTCTAGAGATGGCTAGTAAAGGATTATCAGGGATACTATCT
ACTAGTATTGGGGAATTAACTCATCTTCATACTTTGTTACTTCAGAATAATCAGTTAACT
GGTCCGATTCCTTCTGAGTTAGGCCAACTCTCTGAGCTTGAAACGCTTGATTTATCGGGG
AATCGGTTTAGTGGTGAAATCCCAGCTTCTTTAGGGTTCTTAACTCACTTAAACTACTTG
CGGCTTAGCAGGAATCTTTTATCTGGGCAAGTCCCTCACCTCGTCGCTGGCCTCTCAGGT
CTTTCTTTCTTGGATCTATCTTTCAACAATCTAAGCGGACCAACTCCGAATATATCAGCA
AAAGATTACAGGAAATGCATTTCTTTGTGGTCCAGCTTCCCAAGAGCTTTGCTCAGATGC
TACACCTGTGAGAAATGCTGCAATCGATCTGCAGCGACGGGTTTGTCTGAAAAGGACAAT
AGCAAACATCACAGCTTAGTGCTCTCTTTTGCATTTGGCATTGTTGTTGCCTTTATCATC
TCCCTAATGTTTCTCTTCTTCTGGGTGCTTTGGCATCGATCACGTCTCTCAAGATCACAC
GTGCAGCAAGACTACGAATTTGAAATCGGCCATCTGAAAAGGTTCAGTTTTCGCGAAATA
CAAACCGCAACAAGCAATTTTAGTCCAAAGAACATTTTGGGACAAGGAGGGTTTGGGATG
GTTTATAAAGGGTATCTCCCAAATGGAACTGTGGTGGCAGTTAAAAGATTGAAAGATCCG
ATTTATACAGGAGAAGTTCAGTTTCAAACCGAAGTAGAGATGATTGGCTTAGCTGTTCAC
CGTAACCTTTTACGCCTCTTTGGATTCTGTATGACCCCGGAAGAGAGAATGCTTGTGTAT
CCGTACATGCCAAATGGAAGCGTAGCTGATCGTCTGAGAGATTGGAATCGGAGGATAAGC
ATTGCACTCGGCGCAGCTCGAGGACTTGTTTACTTGCACGAGCAATGCAATCCAAAGATT
ATTCACAGAGACGTCAAAGCTGCAAATATTCTACTTGATGAGAGCTTTGAAGCAATAGTT
GGCGATTTTGGTCTAGCAAAGCTTTTAGACCAGAGAGATTCACATGTCACTACCGCAGTC
CGAGGAACCATTGGACACATCGCTCCCGAGTACCTTTCCACTGGACAGTCCTCAGAGAAA
ACCGATGTTTTCGGATTCGGAGTACTAATCCTTGAACTCATAACAGGTCATAAGATGATT
GATCAAGGCAATGGTCAAGTTCGAAAAGGAATGATATTGAGCTGGGTAAGGACATTGAAA
GCAGAGAAGAGATTTGCAGAGATGGTGGACAGAGATTTGAAGGGAGAGTTTGATGATTTG
GTGTTGGAGGAAGTAGTGGAATTGGCTTTGCTTTGTACACAGCCACATCCGAATCTAAGA
CCGAGGATGTCTCAAGTGTTGAAGGTACTAGAAGGTTTAGTGGAACAGTGTGAAGGAGGG
TATGAAGCTAGAGCTCCAAGTGTCTCTAGGAACTACAGTAATGGTCATGAAGAGCAGTCC
TTTATTATTGAAGCCATTGAGCTCTCTGGACCACGATGAtagacttcatagtgtcttaac

tagtcttcttgattttgttgtcattgtcatggc

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS5 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains no leucine zipper motif, in contrast to the other RKS proteins. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine residues, and is likely to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eight domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

MEISLMKFLFLGIWVYYYS
VLDSVSAMDSLLSPKV

AALMSVKNKMKDE
KEVLSGWDINSVD

PCTWNMVGCSSEGFVVS

LEMASKGLSGILS
T SIGELTHLHTLLLQNNQLTGPI
PSELGQLSELETLDLSGNRFSGEI
PASLGFLTHLNYLRLSRNLLSGQV

PHLVAGLSGLSFLDLSFNNLSGPT
PNISAK DYRKCISLWSSFPR

ALLRCYTCEKCCNR
SAATGLSEKDNSK

HHSLVLSFAFGIVV
AFIISLMFLFFWVLWH

RSRLSRSHVQQDYEF
EIGHLKRFSFREIQTAT

SNFSPKNILGQGGFGMVYKGYLPN
GTVVAVKRLKDPIYTGEVQFQ
TEVEMIGLAVHRNLLRLFGFCM
TPEERMLVYPYMPNGSVADRLR
DWNRRISIALGAA
RGLVYLHEQCNPKIIHRDVKAA
NILLDESFEAIVGDFGLAKLLD
QRDSHVTTAVRGTIGHIAPEYL
STGQSSEKTDVFGFGVLILELI
TGHKMIDQGNGQVRKGMILSW
VRTLKAEKRFAEMVDRDLKGEF
DDLVLEEVVELALLCTQPHPNL
RPRMSQVLKV

LEGLVEQCEGGYEARA

PASVSRNYSNGHEEQSFIIEAIELSGPR

Arabidopsis thaliana RKS6 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.
The first stopcodon has been underlined.
Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

attgtttccttcttttgggattttctccttggatggaaccagctcaattaatgagatgag
ATGAGAATGTTCAGCTTGCAGAAGATGGCTATGGCTTTTACTCTCTTGTTTTTTGCCTGT
TTATGCTCATTTGTGTCTCCAGATGCTCAAGGGGATGCACTGTTTGCGTTGAGGATCTCC
TTACGTGCATTACCGAATCAGCTAAGTGACTGGAATCAGAACCAAGTTAATCCTTGCACT
TGGTCCCAAGTTATTTGTGATGACAAAAACTTTGTCACTTCTCTTACATTGTCAGATATG
AACTTCTCGGGAACCTTGTCTTCAAGAGTAGGAATCCTAGAAAATCTCAAGACTCTTACT
TTAAAGGGAAATGGAATTACGGGTGAAATACCAGAAGACTTTGGAAATCTGACTAGCTTG
ACTAGTTTGGATTTGGAGGACAATCAGCTAACTGGTCGTATACCATCCACTATCGGTAAT
CTCAAGAAACTTCAGTTCTTGACCTTGAGTAGGAACAAACTTAATGGGACTATTCCGGAG
TCACTCACTGGTCTTCCAAACCTGTTAAACCTGCTGCTTGATTCCAATAGTCTCAGTGGT
CAGATTCCTCAAAGTCTGTTTGAGATCCCAAAATATAATTTCACGTCAAACAACTTGAAT
TGTGGCGGTCGTCAACCTCACCCTTGTGTATCCGCGGTTGCCCATTCAGGTGATTCAAGC
AAGCCTAAAACTGGCATTATTGCTGGAGTTGTTGCTGGAGTTACAGTTGTTCTCTTTGGA
ATCTTGTTGTTTCTGTTCTGCAAGGATAGGCATAAAGGATATAGACGTGATGTGTTTGTG
GATGTTGCAGGTGAAGTGGACAGGAGAATTGCATTTGGACAGTTGAAAAGGTTTGCATGG
AGAGAGCTCCAGTTAGCGACAGATAACTTCAGCGAAAAGAATGTACTTGGTCAAGGAGGC
TTTGGGAAAGTTTACAAAGGAGTGCTTCCGGATACACCCAAAGTTGCTGTGAAGAGATTG
ACGGATTTCGAAAGTCCTGGTGGAGATGCTGCTTTCCAAAGGGAAGTAGAGATGATAAGT
GTAGCTGTTCATAGGAATCTACTCCGTCTTATCGGGTTCTGCACCACACAAACAGAACGC
CTTTTGGTTTATCCCTTCATGCAGAATCTAAGTCTTGCACATCGTCTGAGAGAGATCAAA
GCAGGCGACCCGGTTCTAGATTGGGAGACGAGGAAACGGATTGCCTTAGGAGCAGCGCGT
GGTTTTGAGTATCTTCATGAACATTGCAATCCGAAGATCATACATCGTGATGTGAAAGCA
GCTAATGTGTTACTAGATGAAGATTTTGAAGCAGTGGTTGGTGATTTTGGTTTAGCCAAG
CTAGTAGATGTTAGAAGGACTAATGTGACTACTCAAGTTCGAGGAACAATGGGTCACATT
GCACCAGAATATTTATCAACAGGGAAATCATCAGAGAGAACCGATGTTTTCGGGTATGGA
ATTATGCTTCTTGAGCTTGTTACAGGACAACGCGCAATAGACTTTTCACGTTTGGAGGAA
GAAGATGATGTCTTGTTACTTGACCACGTGAAGAAACTGGAAAGAGAGAAGAGATTAGGA
GCAATCGTAGATAAGAATTTGGATGGAGAGTATATAAAAGAAGAAGTAGAGATGATGATA
CAAGTGGCTTTGCTTTGTACACAAGGTTCACCAGAAGACCGACCAGTGATGTCTGAAGTT
GTGAGGATGTTAGAAGGAGAAGGGCTTGCGGAGAGATGGGAAGAGTGGCAAAACGTGGAA
GTCACGAGACGTCATGAGTTTGAACGGTTGCAGAGGAGATTTGATTGGGGTGAAGATTCT
ATGCATAACCAAGATGCCATTGAATTATCTGGTGGAAGA<u>TGA</u>ccaaaaacatcaaacctt

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS6 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 3 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eight domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

MRMFSL
QKMAMAFTLLFFACLCSFVSPDAQG

DALFALRISLRALP
NQLSDWNQNQVN

PCTWSQVICDDKNFVTSL

TLSDMNFSGTLSSRV
GILENLKTLTLKGNGITGEI
PEDFGNLTSLTSLDLEDNQLTGRI

PSTIGNLKKLQFLTLSRNKLNGTI
PESLTGLPNLLNLLLDSNSLSGQI
PQSLFEIPKYNFTSNNLNCGG

RQPHPCVSAVAHSGDSSKPKTG

IIAGVVAGVTVVL
FGILLFLFC

KDRHKGYRRDVFVDVAGE
VDRRIAFGQLKRFAWRELQLAT

DNFSEKNVLGQGGFGKVYKGVLPD
TPKVAVKRLTDFESPGGDAAFQ
REVEMISVAVHRNLLRLIGFCT
TQTERLLVYPFMQNLSLAHRLR
EIKAGDPVLDWETRKRIALGAA
RGFEYLHEHCNPKIIHRDVKAA
NVLLDEDFEAVVGDFGLAKLVD
VRRTNVTTQVRGTMGHIAPEYL
STGKSSERTDVFGYGIMLLELV
TGQRAIDFSRLEEEDDVLLLDH
VKKLEREKRLGAIVDKNLDGEY
IKEEVEMMIQVALLCTQGSPED
RPVMSEVVRMLE

GEGLAERWEEWQNVEVTRRHEFE

RLQRRFDWGEDSMHNQDAIELSGGR

Arabidopsis thaliana RKS7 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

acatcttgttttctgctcattcctctgtttcaaca**ATG**GAGAGTACTATTGTTATGATGA
TGATGATAACAAGATCTTTCTTTTGCTTCTTGGGATTTTTATGCCTTCTCTGCTCTTCTG
TTCACGGATTGCTTTCTCCTAAAGGTGTTAACTTTGAAGTGCAAGCTTTGATGGACATAA
AAGCTTCATTACATGATCCTCATGGTGTTCTTGATAACTGGGATAGAGATGCTGTTGATC
CTTGTAGTTGGACAATGGTCACTTGTTCTTCTGAAAACTTTGTCATTGGCTTAGGCACAC
CAAGTCAGAATTTATCTGGTACACTATCTCCAAGCATTACCAACTTAACAAATCTTCGGA
TTGTGCTGTTGCAGAACAACAACATAAAAGGAAAAATTCCTGCTGAGATTGGTCGGCTTA
CGAGGCTTGAGACTCTTGATCTTTCTGATAATTTCTTCCACGGTGAAATTCCTTTTTCAG
TAGGCTATCTACAAAGCCTGCAATATCTGAGGCTTAACAACAATTCTCTCTCTGGAGTGT
TTCCTCTGTCACTATCTAATATGACTCAACTTGCCTTTCTTGATTTATCATACAACAATC
TTAGTGGTCCTGTTCCAAGATTTGCTGCAAAGACGTTTAGCATCGTTGGGAACCCGCTGA
TATGTCCAACGGGTACCGAACCAGACTGCAATGGAACAACATTGATACCTATGTCTATGA
ACTTGAATCAAACTGGAGTTCCTTTATACGCCGGTGGATCGAGGAATCACAAAATGGCAA
TCGCTGTTGGATCCAGCGTTGGGACTGTATCATTAATCTTCATTGCTGTTGGTTTGTTTC
TCTGGTGGAGACAAAGACATAACCAAAACACATTCTTTGATGTTAAAGATGGGAATCATC
ATGAGGAAGTTTCACTTGGAAACCTGAGGAGATTTGGTTTCAGGGAGCTTCAGATTGCGA
CCAATAACTTCAGCAGTAAGAACTTATTGGGGAAAGGTGGCTATGGAAATGTATACAAAG
GAATACTTGGAGATAGTACAGTGGTTGCAGTGAAAAGGCTTAAAGATGGAGGAGCATTGG
GAGGAGAGATTCAGTTTCAGACAGAAGTTGAAATGATCAGTTTAGCTGTTCATCGAAATC
TCTTAAGACTCTACGGTTTCTGCATCACACAAACTGAGAAGCTTCTAGTTTATCCTTATA
TGTCTAATGGAAGCGTTGCATCTCGAATGAAAGCAAAACCTGTTCTTGACTGGAGCATAA
GGAAGAGGATAGCCATAGGAGCTGCAAGAGGGCTTGTGTATCTCCATGAGCAATGTGATC
CGAAGATTATCCACCGCGATGTCAAAGCAGCGAATATACTTCTTGATGACTACTGTGAAG
CTGTGGTTGGCGATTTTGGTTTAGCTAAACTCTTGGATCATCAAGATTCTCATGTGACAA
CCGCGGTTAGAGGCACGGTGGGTCACATTGCTCCAGAGTATCTCTCAACTGGTCAATCCT
CTGAGAAAACAGATGTTTTTGGCTTCGGGATTCTTCTTCTTGAGCTTGTAACCGGACAAA
GAGCTTTTGAGTTTGGTAAAGCGGCTAACCAGAAAGGTGTGATGCTTGATTGGGTTAAAA
AGATTCATCAAGAGAAGAAACTTGAGCTACTTGTGGATAAAGAGTTGTTGAAGAAGAAGA
GCTACGATGAGATTGAGTTAGACGAAATGGTAAGAGTAGCTTTGTTGTGCACACAGTACC
TGCCAGGACATAGACCAAAAATGTCTGAAGTTGTTCGAATGCTGGAAGGAGATGGACTTG
CAGAGAAATGGGAAGCTTCTCAAAGATCAGACAGTGTTTCAAAATGTAGCAACAGGATAA

ATGAATTGATGTCATCTTCAGACAGATACTCTGATCTTACCGATGACTCTAGTTTACTTG
TGCAAGCAATGGAGCTCTCTGGTCCTAGATGAaatctatacatgaatctgaagaagaaga
agaacatgcatctgtttcttgaatcaagagggattcttgttttttttgtataatagagagg
ttttttggagggaaatgttgtgtctctgtaactgtataggcttgttgtgtaagaagttat
tactgcacttagggttaattcaaagttctttacataaaaaatgattagttgcgttgaata
gagggaacactttgggagatttcatgtatgaaatttggaaaaaaaaaaaaaaaaaaa

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS7 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 3 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eight domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

MESTIVMMMMITRSFF
CFLGFLCLLCSSVHGLLSPKGVNFEV

QALMDIKASLHDP
HGVLDNWDRDAVD

PCSWTMVTCSSENFVIG

LGTPSQNLSGTL
SPSITNLTNLRIVLLQNNNIKGKI
PAEIGRLTRLETLDLSDNFFHGEI
PFSVGYLQSLQYLRLNNNSLSGVF
PLSLSNMTQLAFLDLSYNNLSGPV
PRFAA KTFSIVGNPLICPT

GTEPDCNGTTLIPMSMNL
NQTGVPLYAGGSRNHKMA

IAVGSSVGTVSLIFIAVGLFLWW

RQRHNQNTFFDVKDGNHHE
EVSLGNLRRFGFRELQIAT

NNFSSKNLLGKGGYGNVYKGILGD
STVVAVKRLKDGGALGGEIQFQ
TEVEMISLAVHRNLLRLYGFCI
TQTEKLLVYPYMSNGSVA
SRMKAKPVLDWSIRKRIAIGAA
RGLVYLHEQCDPKIIHRDVKAA
NILLDDYCEAVVGDFGLAKLLD
HQDSHVTTAVRGTVGHIAPEYL
STGQSSEKTDVFGFGILLLELV
TGQRAFEFGKAANQKGVMLDW
VKKIHQEKKLELLVDKELLKKKSY
DEIELDEMVRVALLCTQYLPGH
RPKMSEVVRMLE

GDGLAEKWEASQRSDS
VSKCSNRINELMSSS

DRYSDLTDDSSLLVQAMELSGPR

Arabidopsis thaliana RKS8 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

gttttttttttttaccctcttggaggatctgggaggagaaatttgctttttttggtaa
ATGGGGAGAAAAAAGTTTGAAGCTTTTGGTTTTGTCTGCTTAATCTCACTGCTTCTTCTG
TTTAATTCGTTATGGCTTGCCTCTTCTAACATGGAAGGTGATGCACTGCACAGTTTGAGA
GCTAATCTAGTTGATCCAAATAATGTCTTGCAAAGCTGGGATCCTACGCTTGTTAATCCG
TGTACTTGGTTTCACGTAACGTGTAACAACGAGAACAGTGTTATAAGAGTCGATCTTGGG
AATGCAGACTTGTCTGGTCAGTTGGTTCCTCAGCTAGGTCAGCTCAAGAACTTGCAGTAC
TTGGAGCTTTATAGTAATAACATAACCGGGCCGGTTCCAAGCGATCTTGGGAATCTGACA
AACTTAGTGAGCTTGGATCTTTACTTGAACAGCTTCACTGGTCCAATTCCAGATTCTCTA
GGAAAGCTATTCAAGCTTCGCTTTCTTCGGCTCAACAATAACAGTCTCACCGGACCAATT
CCCATGTCATTGACTAATATCATGACCCTTCAAGTTTTGGATCTGTCGAACAACCGATTA
TCCGGATCTGTTCCTGATAATGGTTCCTTCTCGCTCTTCACTCCCATCAGTTTTGCTAAC
AACTTGGATCTATGCGGCCCAGTTACTAGCCGTCCTTGTCCTGGATCTCCCCCGTTTTCT
CCTCCACCACCTTTTATACCACCTCCCATAGTTCCTACACCAGGTGGGTATAGTGCTACT
GGAGCCATTGCGGGAGGAGTTGCTGCTGGTGCTGCTTTACTATTTGCTGCCCCTGCTTTA
GCTTTTGCTTGGTGGCGTAGAAGAAAACCTCAAGAATTCTTCTTTGATGTTCCTGCCGAA
GAGGACCCTGAGGTTCACTTGGGGCAGCTTAAGCGGTTCTCTCTACGGGAACTTCAAGTA
GCAACTGATAGCTTCAGCAACAAGAACATTTTGGGCCGAGGTGGGTTCGGAAAAGTCTAC
AAAGGCCGTCTTGCTGATGGAACACTTGTTGCAGTCAAACGGCTTAAAGAAGAGCGAACC
CCAGGTGGCGAGCTCCAGTTTCAGACAGAAGTGGAGATGATAAGCATGGCCGTTCACAGA
AATCTCCTCAGGCTACGCGGTTTCTGTATGACCCCTACCGAGAGATTGCTTGTTTATCCT
TACATGGCTAATGGAAGTGTCGCTTCCTGTTTGAGAGAACGTCCACCATCACAGTTGCCT
CTAGCCTGGTCAATAAGACAGCAAATCGCGCTAGGATCAGCGAGGGGTTTGTCTTATCTT
CATGATCATTGCGACCCCAAAATTATTCACCGTGATGTGAAAGCTGCTAATATTCTGTTG
GACGAGGAATTTGAGGCGGTGGTAGGTGATTTCGGGTTAGCTAGACTTATGGACTATAAA
GATACTCATGTCACAACGGCTGTGCGTGGGACTATTGGACACATTGCTCCTGAGTATCTC
TCAACTGGAAAATCTTCAGAGAAAACTGATGTTTTTGGCTACGGGATCATGCTTTTGGAA
CTGATTACAGGTCAGAGAGCTTTTGATCTTGCAAGACTGGCGAATGACGATGACGTTATG
CTCCTAGATTGGGTGAAAGGGCTTTTGAAGGAGAAGAAGCTGGAGATGCTTGTGGATCCT
GACCTGCAAAGCAATTACACAGAAGCAGAAGTAGAACAGCTCATACAAGTGGCTCTTCTC
TGCACACAGAGCTCACCTATGGAACGACCTAAGATGTCTGAGGTTGTTCGAATGCTTGAA
GGTGACGGTTTAGCGGAGAAATGGGACGAGTGGCAGAAAGTGGAAGTTCTCAGGCAAGAA

GTGGAGCTCTCTTCTCACCCCACCTCTGACTGGATCCTTGATTCGACTGATAATCTTCAT
GCTATGGAGTTGTCTGGTCCAAGATAAacgacattgtaatttgcctaacagaaaagagaa
agaacagagaaatattaagagaatcacttctctgtattctt

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS8 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt *et al.* (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 4 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eight domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

MGRKKFEAFGFVCLISLLLLFNSL
WLASSNMEG

DALHSLRANLVDP
NNVLQSWDPTLVN

PCTWFHVTCNNENSVIRV

DLGNADLSGQLV
P QLGQLKNLQYLELYSNNITGPV
PSDLGNLTNLVSLDLYLNSFTGPI

PDSLGKLFKLRFLRLNNNSLTGPI
PMSLTNIMTLQVLDLSNNRLSGSV
PDNGSFSLFTPISFANNLDLCGPV

TSRPCPGSPPFSPPPP
FIPPPIVPTPGGYSATG

AIAGGVAAGAAL
LFAAPALAFAWW

RRRKPQEFFFDVPAEEDPE
VHLGQLKRFSLRELQVAT

DSFSNKNILGRGGFGKVYKGRLAD
GTLVAVKRLKEERTPGGELQFQ
TEVEMISMAVHRNLLRLRGFCM
TPTERLLVYPYMANGSVASCLR
ERPPSQLPLAWSIRQQIALGSA
RGLSYLHDHCDPKIIHRDVKAA
NILLDEEFEAVVGDFGLARLMD
YKDTHVTTAVRGTIGHIAPEYL
STGKSSEKTDVFGYGIMLLELI
TGQRAFDLARLANDDDVMLLDW
VKGLLKEKKLEMLVDPDLQSNY
TEAEVEQLIQVALLCTQSSPME
RPKMSEVVRMLE

GDGLAEKWDEWQKVEVLRQEVELS

SHPTSDWILDSTDNLHAMELSGPR

Arabidopsis thaliana rks10 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

atcaggggttttaacaatgatggattttctctgatgagggatagttctagggtttgtttt
taatctcttgaggataaa**ATG**GAACGAAGATTAATGATCCCTTGCTTCTTTTGGTTGATT
CTCGTTTTGGATTTGGTTCTCAGAGTCTCGGGCAACGCCGAAGGTGATGCTCTAAGTGCA
CTGAAAAACAGTTTAGCCGACCCTAATAAGGTGCTTCAAAGTTGGGATGCTACTCTTGTT
ACTCCATGTACATGGTTTCATGTTACTTGCAATAGCGACAATAGTGTTACACGTGTTGAC
CTTGGGAATGCAAATCTATCTGGACAGCTCGTAATGCAACTTGGTCAGCTTCCAAACTTG
CAGTACTTGGAGCTTTATAGCAATAACATTACTGGGACAATCCCAGAACAGCTTGGAAAT
CTGACGGAATTGGTGAGCTTGGATCTTTACTTGAACAATTTAAGCGGGCCTATTCCATCA
ACTCTCGGCCGACTTAAGAAACTCCGTTTCTTGCGTCTTAATAACAATAGCTTATCTGGA
GAAATTCCAAGGTCTTTGACTGCTGTCCTGACGCTACAAGTTCTGGATCTCTCAAACAAT
CCTCTCACCGGAGATATTCCTGTTAATGGTTCCTTTTCACTTTTCACTCCAATCAGTTTT
GCCAACACCAAGTTGACTCCCCTTCCTGCATCTCCACCGCCTCCTATCTCTCCTACACCG
CCATCACCTGCAGGGAGTAATAGAATTACTGGAGCGATTGCGGGAGGAGTTGCTGCAGGT
GCTGCACTTCTATTTGCTGTTCCGGCCATTGCACTAGCTTGGTGGCGAAGGAAAAAGCCG
CAGGACCACTTCTTTGATGTACCAGCTGAAGAGGACCCAGAAGTTCATTTAGGACAACTG
AAGAGGTTTTCATTGCGTGAACTACAAGTTGCTTCGGATAATTTTAGCAACAAGAACATA
TTGGGTAGAGGTGGTTTTGGTAAAGTTTATAAAGGACGGTTAGCTGATGGTACTTTAGTG
GCCGTTAAAAGGCTAAAAGAGGAGCGCACCCAAGGTGGCGAACTGCAGTTCCAGACAGAG
GTTGAGATGATTAGTATGGCGGTTCACAGAAACTTGCTTCGGCTTCGTGGATTTTGCATG
ACTCCAACCGAAAGATTGCTTGTTTATCCCTACATGGCTAATGGAAGTGTTGCCTCCTGT
TTAAGAGAACGTCCCGAGTCCCAGCCACCACTTGATTGGCCAAAGAGACAGCGTATTGCG
TTGGGATCTGCAAGAGGGCTTGCGTATTTACATGATCATTGCGACCCAAAGATTATTCAT
CGAGATGTGAAAGCTGCAAATATTTTGTTGGATGAAGAGTTTGAAGCCGTGGTTGGGGAT
TTTGGACTTGCAAAACTCATGGACTACAAAGACACACATGTGACAACCGCAGTGCGTGGG
ACAATTGGTCATATAGCCCCTGAGTACCTTTCCACTGGAAAATCATCAGAGAAAACCGAT
GTCTTTGGGTATGGAGTCATGCTTCTTGAGCTTATCACTGGACAAAGGGCTTTTGATCTT
GCTCGCCTCGCGAATGATGATGATGTCATGTTACTAGACTGGGTGAAAGGGTTGTTAAAA
GAGAAGAAATTGGAAGCACTAGTAGATGTTGATCTTCAGGGTAATTACAAAGACGAAGAA
GTGGAGCAGCTAATCCAAGTGGCTTTACTCTGCACTCAGAGTTCACCAATGGAAAGACCC
AAAATGTCTGAAGTTGTAAGAATGCTTGAAGGAGATGGTTTAGCTGAGAGATGGGAAGAG
TGGCAAAAGGAGGAAATGTTCAGACAAGATTTCAACTACCCAACCCACCATCCAGCCGTG

TCTGGCTGGATCATTGGCGATTCCACTTCCCAGATCGAAAACGAATACCCCTCGGGTCCA
AGATAAgattcgaaacacgaatgttttttctgtattttgtttttctctgtatttattgag
ggttttagcttc

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS10 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt *et al.* (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 4 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eight domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

MERRLMIPCFFWLILVL
DLVLRVSGNAEG

DALSALKNSLADP
NKVLQSWDATLVT

PCTWFHVTCNSDNSVTRV

DLGNANLSGQLV
M QLGQLPNLQYLELYSNNITGTI
PEQLGNLTELVSLDLYLNNLSGPI

PSTLGRLKKLRFLRLNNNSLSGEI
PRSLTAVLTLQVLDLSNNPLTGDI
PVNGSFSLTPISFANTK LT PL

PASPPPPISPTPPSPAGSNRITG

AIAGGVAAGAAL
LFAVPAIALAWW

RRKKPQDHFFDVPAEEDPE
VHLGQLKRFSLRELQVAS

DNFSNKNILGRGGFGKVYKGRLAD
GTLVAVKRLKEERTQGGELQFQ
TEVEMISMAVHRNLLRLRGFCM
TPTERLLVYPYMANGSVASCLR
ERPESQPPLDWPKRQRIALGSA
RGLAYLHDHCDPKIIHRDVKAA
NILLDEEFEAVVGDFGLAKLMD
YKDTHVTTAVRGTIGHIAPEYL
STGKSSEKTDVFGYGVMLLELI
TGQRAFDLARLANDDDVMLLDW
VKGLLKEKKLEALVDVDLQGNY
KDEEVEQLIQVALLCTQSSPME
RPKMSEVVRMLE

GDGLAERWEEWQKEEMFRQDFNYPTHH

PAVSGWIIGDSTSQIENEYPSGPR

Arabidopsis thaliana RKS 11 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

ttgttaacctctcgtaactaaaatcttcc**ATG**GTAGTAGTAACAAAGAAGACCATGAAGA
TTCAAATTCATCTCCTTTACTCGTTCTTGTTCCTCTGTTTCTCTACTCTCACTCTATCTT
CTGAGCCCAGAAACCCTGAAGTTGAGGCGTTGATAAGTATAAGGAACAATTTGCATGATC
CTCATGGAGCTTTGAACAATTGGGACGAGTTTTCAGTTGATCCTTGTAGCTGGGCTATGA
TCACTTGCTCTCCCGACAACCTCGTCATTGGACTAGGAGCGCCGAGCCAGTCTCTCTCGG
GAGGTTTATCTGAGTCTATCGGAAATCTCACAAATCTCCGACAAGTGTCATTGCAAAATA
ACAACATCTCCGGCAAAATTCCACCGGAGCTCGGTTTTCTACCCAAATTACAAACCTTGG
ATCTTTCCAACAACCGATTCTCCGGTGACATCCCTGTTTCCATCGACCAGCTAAGCAGCC
TTCAATATCTGAGACTCAACAACAACTCTTTGTCTGGGCCCTTCCCTGCTTCTTTGTCCC
AAATTCCTCACCTCTCCTTCTTGGACTTGTCTTACAACAATCTCAGTGGCCCTGTTCCTA
AATTCCCAGCAAGGACTTTAAACGTTGCTGGTAATCCTTTGATTTGTAGAAGCAACCCAC
CTGAGATTTGTTCTGGATCAATCAATGCAAGTCCACTTTCTGTTTCTTTGAGCTCTTCAT
CAGGACGCAGGTCTAATAGATTGGCAATAGCTCTTAGTGTAAGCCTTGGCTCTGTTGTTA
TACTAGTCCTTGCTCTCGGGTCCTTTTGTTGGTACCGAAAGAAACAAAGAAGGCTACTGA
TCCTTAACTTAAACGCAGATAAACAAGAGGAAGGGCTTCAAGGACTTGGGAATCTAAGAA
GCTTCACATTCAGAGAACTCCATGTTTATACAGATGGTTTCAGTTCCAAGAACATTCTCG
GCGCTGGTGGATTCGGTAATGTGTACAGAGGCAAGCTTGGAGATGGGACAATGGTGGCAG
TGAAACGGTTGAAGGATATTAATGGAACCTCAGGGGATTCACAGTTTCGTATGGAGCTAG
AGATGATTAGCTTAGCTGTTCATAAGAATCTGCTTCGGTTAATTGGTTATTGCGCAACTT
CTGGTGAAAGGCTTCTTGTTTACCCTTACATGCCTAATGGAAGCGTCGCCTCTAAGCTTA
AATCTAAACCGGCATTGGACTGGAACATGAGGAAGAGGATAGCAATTGGTGCAGCGAGAG
GTTTGTTGTATCTACATGAGCAATGTGATCCCAAGATCATTCATAGAGATGTAAAGGCAG
CTAATATTCTCTTAGACGAGTGCTTTGAAGCTGTTGTTGGTGACTTTGGACTCGCAAAGC
TCCTTAACCATGCGGATTCTCATGTCACAACTGCGGTCCGTGGTACGGTTGGCCACATTG
CACCTGAATATCTCTCCACTGGTCAGTCTTCTGAGAAAACCGATGTGTTTGGGTTCGGTA
TACTATTGCTCGAGCTCATAACCGGACTGAGAGCTCTTGAGTTTGGTAAAACCGTTAGCC
AGAAAGGAGCTATGCTTGAATGGGTGAGGAAATTACATGAAGAGATGAAAGTAGAGGAAC
TATTGGATCGAGAACTCGGAACTAACTACGATAAGATTGAAGTTGGAGAGATGTTGCAAG
TGGCTTTGCTATGCACACAATATCTGCCAGCTCATCGTCCTAAAATGTCTGAAGTTGTTT
TGATGCTTGAAGGCGATGGATTAGCCGAGAGATGGGCTGCTTCGCATAACCATTCACATT
TCTACCATGCCAATATCTCTTTCAAGACAATCTCTTCTCTGTCTACTACTTCTGTCTCAA

GGCTTGACGCACATTGCAATGATCCAACTTATCAAATGTTTGGATCTTCGGCTTTCGATG
ATGACGATGATCATCAGCCTTTAGATTCCTTTGCCATGGAACTATCCGGTCCAAGATAAc
acaatgaaagaaagatatcatttttacgatggatcaaacaatccaatgaaaaaa

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS11 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt *et al.* (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 3 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eight domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

MVVVTKKTMKIQIHLLYSFLFL
CFSTLTLSSEPRNPEV

EALISIRNNLHDP
HGALNNWDEFSVD

PCSWAMITCSPDNLVIGL

GAPSQSLSGGLS
ESIGNLTNLRQVSLQNNNISGKI
PPELGFLPKLQTLDLSNNRFSGDI
PVSIDQLSSLQYLRLNNNSLSGPF
PASLSQIPHLSFLDLSYNNLSGPV
PKFPARTFNVAGNPLICRSN

PPEICSGSINASPL
SVSLSSSSGRRSNR

LAIALSVSLGSVVIL
VLALGSFCWY

RKKQRRLLILNLNGADKQEE
GLQGLGNLRSFTFRELHVYT

DGFSSKNILGAGGFGNVYRGKLGD
GTMVAVKRLKDINGTSGDSQFR
MELEMISLAVHKNLLRLIGYCA
TSGERLLVYPYMPNGSVASKLK
SKPALDWNMRKRIAIGAA
RGLLYLHEQCDPKIIHRDVKAA
NILLDECFEAVVGDFGLAKLLN
HADSHVTTAVRGTVGHIAPEYL
STGQSSEKTDVFGFGILLLELI
TGLRALEFGKTVSQKGAMLEW
VRKLHEEMKVEELLDRELGTNY
DKIEVGEMLQVALLCTQYLPAH
RPKMSEVVLMLE

GDGLAERWAASHNHSHFYHANI
SFKTISSLSTTSVSRLDAHCNDPTYQMFG

SSAFDDDDDHQPLDSFAMELSGPR

Arabidopsis thaliana RKS12 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

tttaaaaaccttgctagttctcaattctcatgactttgcttttagtcttagaagtggaaa
ATGGAACATGGATCATCCCGTGGCTTTATTTGGCTGATTCTATTTCTCGATTTTGTTTCC
AGAGTCACCGGAAAAACACAAGTTGATGCTCTCATTGCTCTAAGAAGCAGTTTATCATCA
GGTGACCATACAAACAATATACTCCAAAGCTGGAATGCCACTCACGTTACTCCATGTTCA
TGGTTTCATGTTACTTGCAATACTGAAAACAGTGTTACTCGTCTTGACCTGGGGAGTGCT
AATCTATCTGGAGAACTGGTGCCACAGCTTGCTCAGCTTCCAAATTTGCAGTACTTGGAA
CTTTTTAACAATAATATTACTGGGGAGATACCTGAGGAGCTTGGCGACTTGATGGAACTA
GTAAGCTTGGACCTTTTTGCAAACAACATAAGCGGTCCCATCCCTTCCTCTCTTGGCAAA
CTAGGAAAACTCCGCTTCTTGCGTCTTTATAACAACAGCTTATCTGGAGAAATTCCAAGG
TCTTTGACTGCTCTGCCGCTGGATGTTCTTGATATCTCAAACAATCGGCTCAGTGGAGAT
ATTCCTGTTAATGGTTCCTTTTCGCAGTTCACTTCTATGAGTTTTGCCAATAATAAATTA
AGGCCGCGACCTGCATCTCCTTCACCATCACCTTCAGGAACGTCTGCAGCAATAGTAGTG
GGAGTTGCTGCGGGTGCAGCACTTCTATTTGCGCTTGCTTGGTGGCTGAGAAGAAAACTG
CAGGGTCACTTTCTTGATGTACCTGCTGAAGAAGACCCAGAGGTTTATTTAGGACAATTT
AAAAGGTTCTCCTTGCGTGAACTGCTAGTTGCTACAGAGAAATTTAGCAAAAGAAATGTA
TTGGGCAAAGGACGTTTTGGTATATTGTATAAAGGACGTTTAGCTGATGACACTCTAGTG
GCTGTGAAACGGCTAAATGAAGAACGTACCAAGGGTGGGGAACTGCAGTTTCAAACCGAA
GTTGAGATGATCAGTATGGCCGTTCATAGGAACTTGCTTCGGCTTCGTGGCTTTTGCATG
ACTCCAACTGAAAGATTACTTGTTTATCCCTACATGGCTAATGGAAGTGTTGCTTCTTGT
TTAAGAGAGCGTCCTGAAGGCAATCCAGCCCTTGACTGGCCAAAAAGAAAGCATATTGCT
CTGGGATCAGCAAGGGGGCTCGCATATTTACACGATCATTGCGACCAAAAGATCATTCAC
CTGGATGTGAAAGCTGCAAATATACTGTTAGATGAAGAGTTTGAAGCTGTTGTTGGAGAT
TTTGGGCTAGCAAAATTAATGAATTATAACGACTCCCATGTGACAACTGCTGTACGGGGT
ACGATTGGCCATATAGCGCCCGAGTACCTCTCGACAGGAAAATCTTCTGAGAAGACTGAT
GTTTTTGGGTACGGGGTCATGCTTCTCGAGCTCATCACTGGACAAAAGGCTTTCGATCTT
GCTCGGCTTGCAAATGATGATGATATCATGTTACTCGACTGGGTGAAAGAGGTTTTGAAA
GAGAAGAAGTTGGAAAGCCTTGTGGATGCAGAACTCGAAGGAAAGTACGTGGAAACAGAA
GTGGAGCAGCTGATACAAATGGCTCTGCTCTGCACTCAAAGTTCTGCAATGGAACGTCCA
AAGATGTCAGAAGTAGTGAGAATGCTGGAAGGAGATGGTTTAGCTGAGAGATGGGAAGAA
TGGCAAAAGGAGGAGATGCCAATACATGATTTTAACTATCAAGCCTATCCTCATGCTGGC
ACTGACTGGCTCATCCCCTATTCCAATTCCCTTATCGAAAACGATTACCCCTCGGGGCCA

AGATAAccttttagaaagggtcatttcttgtgggttcttcaacaagtatatatataggta
gtgaagttgtaagaagcaaaaccccacattcacctttgaatatcactactctataa

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS12 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt *et al.* (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 2 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eight domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

MEHGSSRGFI
WLILFLDFVSRVTGKTQV

DALIALRSSLSSGDHTNNILQ
SWNATHVT

PCSWFHVTCNTENSVTRL

DLGSANLSGELV
P QLAQLPNLQYLELFNNNITGEI
PEELGDLMELVSLDLFANNISGPI
PSSLGKLGKLRFLRLYNNSLSGEI
PRSLTALP LDVLDISNNRLSGDI
PVNGSFSQFTSMRFA NNKLRPR

PASPSPSPSGGTS

AAIVVGVAAGAALLFALAWWL

RRKLQGHFLDVPAAEEDPE
VYLGQFKRFSLRELLVAT

EKFSKRNVLGKGRFGILYKGRLAD
DTLVAVKRLNEERTKGGELQFQ
TEVEMISMAVHRNLLRLRGFCM
TPTERLLVYPYMANGSVASCLR
ERPEGNPALDWPKRKHIALGSA
RGLAYLHDHCDQKIIHLDVKAA
NILLDEEFEAVVGDFGLAKLMN
YNDSHVTTAVRGTIGHIAPEYL
STGKSSEKTDVFGYGVMLLELI
TGQKAFDLARLANDDDIMLLDW
VKEVLKEKKLESLVDAELEGKY
VETEVEQLIQMALLCTQSSAME
RPKMSEVVRMLE

GDGLAERWEEWQKEEMPIHDFNYQAY

PHAGTDWLIPYSNSLIENDYPSGPR

Arabidopsis thaliana RKS13 cDNA

The start codons encoding predicted the methionine residue of the gene product has been indicated by bold capitals. The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

taataaacctctaataataatggctttgcttttactctgatgacaagttcaaaaATGGAA
CAAAGATCACTCCTTTGCTTCCTTTATCTGCTCCTACTATTCAATTTCACTCTCAGAGTC
GCTGGAAACGCTGAAGGTGATGCTTTGACTCAGCTGAAAAACAGTTTGTCATCAGGTGAC
CCTGCAAACAATGTACTCCAAAGCTGGGATGCTACTCTTGTTACTCCATGTACTTGGTTT
CATGTTACTTGCAATCCTGAGAATAAAGTTACTCGTGTTGACCTTGGGAATGCAAAACTA
TCTGGAAAGTTGGTTCCAGAACTTGGTCAGCTTTTAAACTTGCAGTACTTGGAGCTTTAT
AGCAATAACATTACAGGGGAGATACCTGAGGAGCTTGGCGACTTGGTGGAACTAGTAAGC
TTGGATCTTTACGCAAACAGCATAAGCGGTCCCATCCCTTCGTCTCTTGGCAAACTAGGA
AAACTCCGGTTCTTGCGTCTTAACAACAATAGCTTATCAGGGGAAATTCCAATGACTTTG
ACTTCTGTGCAGCTGCAAGTTCTGGATATCTCAAACAATCGGCTCAGTGGAGATATTCCT
GTTAATGGTTCTTTTTCGCTCTTCACTCCTATCAGTTTTGCGAATAATAGCTTAACGGAT
CTTCCCGAACCTCCGCCTACTTCTACCTCTCCTACGCCACCACCACCTTCAGGGGGGCAA
ATGACTGCAGCAATAGCAGGGGGAGTTGCTGCAGGTGCAGCACTTCTATTTGCTGTTCCA
GCCATTGCGTTTGCTTGGTGGCTCAGAAGAAAACCACAGGACCACTTTTTTGATGTACCT
GCTGAAGAAGACCCAGAGGTTCATTTAGGACAACTCAAAAGGTTTACCTTGCGTGAACTG
TTAGTTGCTACTGATAACTTTAGCAATAAAAATGTATTGGGTAGAGGTGGTTTTGGTAAA
GTGTATAAAGGACGTTTAGCCGATGGCAATCTAGTGGCTGTCAAAAGGCTAAAAGAAGAA
CGTACCAAGGGTGGGGAACTGCAGTTTCAAACCGAAGTTGAGATGATCAGTATGGCCGTT
CATAGGAACTTGCTTCGGCTTCGTGGCTTTTGCATGACTCCAACTGAAAGATTACTTGTT
TATCCCTACATGGCTAATGGAAGTGTTGCTTCTTGTTTAAGAGAGCGTCCTGAAGGCAAT
CCAGCACTTGATTGGCCAAAAAGAAAGCATATTGCTCTGGGATCAGCAAGGGGGCTTGCG
TATTTACATGATCATTGCGACCAAAAAATCATTCACCGGGATGTTAAAGCTGCTAATATA
TTGTTAGATGAAGAGTTTGAAGCTGTTGTTGGAGATTTTGGGCTCGCAAAATTAATGAAT
TATAATGACTCCCATGTGACAACTGCTGTACGCGGTACAATTGGCCATATAGCGCCCGAG
TACCTCTCGACAGGAAAATCTTCTGAGAAGACTGATGTTTTTGGGTACGGGGTCATGCTT
CTCGAGCTCATCACTGGACAAAAGGCTTTCGATCTTGCTCGGCTTGCAAATGATGATGAT
ATCATGTTACTCGACTGGGTGAAAGAGGTTTTGAAAGAGAAGAAGTTGGAAAGCCTTGTG
GATGCAGAACTCGAAGGAAAGTACGTGGAAACAGAAGTGGAGCAGCTGATACAAATGGCT
CTGCTCTGCACTCAAAGTTCTGCAATGGAACGTCCAAAGATGTCAGAAGTAGTGAGAATG
CTGGAAGGAGATGGTTTAGCTGAGAGATGGGAAGAATGGCAAAAGGAGGAGATGCCAATA
CATGATTTTAACTATCAAGCCTATCCTCATGCTGGCACTGACTGGCTCATCCCCTATTCC
AATTCCCTTATCGAAAACGATTACCCCTCGGGTCCAAGATAAcctttagaaagggtctt

ttcttgtgggttcttcaacaagtatatatatagattggtgaagttttaagatgcaaaaaa
aa

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS13 protein.
Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt *et al.* (1997).
At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains leucine zipper motifs, containing 2 times 2 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eight domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

MEQRSLLCFLYLL
LLFNFTLRVAGNAEG

DALTQLKNSLSSGDP
ANNVLQSWDATLVT

PCTWFHVTCNPENKVTRV

DLGNAKLSGKLV
P ELGQLLNLQYLELYSNNITGEI
PEELGDLVELVSLDLYANSISGPI
PSSLGKLGKLRFLRLNNNSLSGEI
PMTLTSVQLQV LDISNNRLSGDI
PVNGSFSLFTPISFANNSLTDLPE

PPPTSTSPTPPPPSG

GQMTAAIAGGVAAGAAL
LFAVPAIAFAWWL

RRKPQDHFFDVPGAEEDPE
VHLGQLKRFTLRELLVAT

DNFSNKNVLGRGGFGKVYKGRLAD
GNLVAVKRLKEERTKGGELQFQ
TEVEMISMAVHRNLLRLRGFCM
TPTERLLVYPYMANGSVASCLR
ERPEGNPALDWPKRKHIALGSA
RGLAYLHDHCDQKIIHRDVKAA
NILLDEEFEAVVGDFGLAKLMN
YNDSHVTTAVRGTIGHIAPEYL
STGKSSEKTDVFGYGVMLLELI
TGQKAFDLARLANDDDIMLLDW
VKEVLKEKKLESLVDAELEGKY
VETEVEQLIQMALLCTQSSAME
RPKMSEVVRMLE

GDGLAERWEEWQKEEMPIHDFNYQA

YPHAGTDWLIPYSNSLIENDYPSGPR

Arabidopsis thaliana RKS14 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

ctgcaccttagagattaatactctcaagaaaaacaagttttgattcggacaaag**ATG**TTG
CAAGGAAGAAGAGAAGCAAAAAAGAGTTATGCTTTGTTCTCTTCAACTTTCTTCTTCTTC
TTTATCTGTTTTCTTTCTTCTTCTTCTGCAGAACTCACAGACAAAGTTGTTGCCTTAATA
GGAATCAAAAGCTCACTGACTGATCCTCATGGAGTTCTAATGAATTGGGATGACACAGCA
GTTGATCCATGTAGCTGGAACATGATCACTTGTTCTGATGGTTTTGTCATAAGGCTAGAA
GCTCCAAGCCAAAACTTATCAGGAACTCTTTCATCAAGTATTGGAAATTTAACAAATCTT
CAAACTGTATACAGGTTATTGCAGAACAATTACATAACAGGAAACATCCCTCATGAGATT
GGGAAATTGATGAAACTCAAAACACTTGATCTCTCTACCAATAACTTCACTGGTCAAATC
CCATTCACTCTTTCTTACTCCAAAAATCTTCACAGGAGGGTTAATAATAACAGCCTGACA
GGAACAATTCCTAGCTCATTGGCAAACATGACCCAACTCACTTTTTTGGATTTGTCGTAT
AATAACTTGAGTGGACCAGTTCCAAGATCACTTGCCAAAACATTCAATGTTATGGGCAAT
TCTCAGATTTGTCCAACAGGAACTGAGAAAGACTGTAATGGGACTCAGCCTAAGCCAATG
TCAATCACCTTGAACAGTTCTCAAAGAACTAAAAACCGGAAAATCGCGGTAGTCTTCGGT
GTAAGCTTGACATGTGTTTGCTTGTTGATCATTGGCTTTGGTTTTCTTCTTTGGTGGAGA
AGAAGACATAACAAACAAGTATTATTCTTTGACATTAATGAGCAAAACAAGGAAGAAATG
TGTCTAGGGAATCTAAGGAGGTTTAATTTCAAAGAACTTCAATCCGCAACTAGTAACTTC
AGCAGCAAGAATCTGGTCGGAAAAGGAGGGTTTGGAAATGTGTATAAAGGTTGTCTTCAT
GATGGAAGTATCATCGCGGTGAAGAGATTAAAGGATATAAACAATGGTGGTGGAGAGGTT
CAGTTTCAGACAGAGCTTGAAATGATAAGCCTTGCCGTCCACCGGAATCTCCTCCGCTTA
TACGGTTTCTGTACTACTTCCTCTGAACGGCTTCTCGTTTATCCTTACATGTCCAATGGC
AGTGTCGCTTCTCGTCTCAAAGCTAAACCGGTATTGGATTGGGGCACAAGAAAGCGAATA
GCATTAGGAGCAGGAAGAGGGTTGCTGTATTTGCATGAGCAATGTGATCCAAAGATCATT
CACCGTGATGTCAAAGCTGCGAACATACTTCTTGACGATTACTTTGAAGCTGTTGTCGGA
GATTTCGGGTTGGCTAAGCTTTTGGATCATGAGGAGTCGCATGTGACAACCGCCGTGAGA
GGAACAGTGGGTCACATTGCACCTGAGTATCTCTCAACAGGACAATCTTCTGAGAAGACA
GATGTGTTCGGTTTCGGGATTCTTCTTCTCGAATTGATTACTGGATTGAGAGCTCTTGAA
TTCGGAAAAGCAGCAAACCAAAGAGGAGCGATACTTGATTGGGTAAAGAAACTACAACAA
GAGAAGAAGCTAGAACAGATAGTAGACAAGGATTTGAAGAGCAACTACGATAGAATAGAA
GTGGAAGAAATGGTTCAAGTGGCTTTGCTTTGTACACAGTATCTTCCCATTCACCGTCCT
AAGATGTCTGAAGTTGTGAGAATGCTTGAAGGCGATGGTCTTGTTGAGAAATGGGAAGCT
TCTTCTCAGAGAGCAGAAACCAATAGAAGTTACAGTAAACCTAACGAGTTTTCTTCCTCT

GAACGTTATTCGGATCTTACAGATGATTCCTCGGTGCTGGTTCAAGCCATGGAGTTATCA
GGTCCAAGATGAcaagagaaactatatgaatggctttgggtttgtaaaaaa

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS14 protein.
Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt *et al.* (1997).
At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 3 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eight domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

MLQGRREAKKSYALFSSTFF
FFFICFLSSSSAELTDKV

VALIGIKSSLTDP
HGVLMNWDDTAVD

PCSWNMITCSDGFVIR

LEAPSQNLSGTLSS
SIGNLTNLQTVYRLLQNNYITGNI
PHEIGKLMKLKTLDLSTNNFTGQI
PFTLSYSKNLHRRV NNNSLTGTI
PSSLANMTQLTFLDLSYNNLSGPV
PRSLAKTFNVMGNSQICPT

GTEKDCNGTQPKPMSITLNSSQR
TKNRK

IAVVFGVSLTCVCLLIIGFGFLLWW

RRRHNKQVLFFDINEQNKE
EMCLGNLRRFNFKELQSAT

SNFSSKNLVGKGGFGNVYKGCLHD
GSIIAVKRLKDINNGGGEVQFQ
TELEMISLAVHRNLLRLYGFCT
TSSERLLVYPYMSNGSVA
SRLKAKPVLDWGTRKRIALGAG
RGLLYLHEQCDPKIIHRDVKAA
NILLDDYFEAVVGDFGLAKLLD
HEESHVTTAVRGTVGHIAPEYL
STGQSSEKTDVFGFGILLLELI
TGLRALEFGKAANQRGAILDW
VKKLQQEKKLEQIVDKDLKSNY
DRIEVEEMVQVALLCTQYLPIH
RPKMSEVVRMLE

GDGLVEKWEASSQRAET
NRSYSKPNEFSSS

ERYSDLTDDSSVLVQAMELSGPR

Legends

Figure 1

The different domains of the predicted RKS gene product have the following functions:
The first domain of the predicted protein structure at the N-terminal end consists of a signal sequence, involved in targeting the protein towards the plasma membrane. Protein cleavage removes this sequence from the final mature protein product (Jain *et al.* 1994, J. Biol. Chemistry 269: 16306-16310). The second domain consists of different numbers of leucine zipper motifs, and is likely to be involved in protein protein dimerization. The next domain contains a conserved pair of cystein residues, involved in disulphate bridge formation. The next domain consists of 5 (or in the case of RKS3 only 4) leucine rich repeats (LRRs) shown in a gray colour, likely to be involved in ligand binding (Kobe and Deisenhofer 1994, TIBS 19: 415-420). This domain is again bordered by a domain containing a conserved pair of cystein residues involved in disulphate bridge formation often followed by a serine /. proline rich region. The next domain displays all the characteristics of a single transmembrane domain (http://genome.cbs.dtu.dk/services/TMHMM/). At the predicted cytoplasmic site of protein a domain is situated with unknown function, followed by a domain with serine /threonine kinase activity (Schmidt et al. 1997, Development 124: 2049-2062). The kinase domain is followed by a domain with unknown function whereas at the C-terminal end of the protein part of a leucine rich repeat is positioned, probably involved in protein-protein interactions.

Figure 2

Alagnment of the predicted protein sequences of the different RKS gene products from *Arabidopsis thaliana* with alignX, Vector NTI Suite 5.5 resulted in a phylogenetic tree in which

the relative homology between the different RKS members is shown.

Figure 3

Intron-Exon bounderies of the genomic regions on the chromosomes of *Arabidopsis thaliana* encoding the different RKS gene products. Exons are shown as boxes, whereas intron sequences are shown as lines. Sequences encoding LRR domains are displayed in gray colour, transmembrane regions in black.

Figure 4.

Cromosomal location of RKS genes in *Arabidopsis thaliana*, showing colocalisation with GASA genes.

Figure 5. A signaling complex comprising molecules of RKS proteins, ELS proteins, NDR/NHL proteins and SBP/SPL proteins.

Figure 6.

Second generation (T2) tobacco seedlings germinated on MS medium. Transformations were performed with DNA clone 2212-15, representing the overexpression construct GT-RKS4-s. T2 seedlings derived from T1 plant 15.7 shows co-suppression effects while T1 plant 15.6 shows no obvious changes in level of RKS4. T1 plants 15.9 and 15.3 show overexpression effects. Plant 15.7 has the lowest remaining level of RKS4 gene product, whereas plant 15.3 has the highest level of RKS4 gene product.

Figure 7

Second generation (T2) tobacco plants. In the upper row the offspring from a co-suppressing T1 plant 15.7 is shown. The middle row shows plants derived from a transgenic T1 plant 15.6 with no clear changes in level of RKS4 is shown while the bottom row shows plants derived from a T1 plant 15.3 in which the levels of RKS4 are increased by the introduction of the overexpression construct GT-RKS4-s.

Figure 8

Second generation (T2) tobacco plants. Plants derived from a co-suppressing T1 plant 15.7 show a reduction in plant size and a delay in the initiation and outgrowth of primordia. The control empty vector transgenic plants show no visible differences in growth compared with the offspring from the transgenic 15.6 plant, in which the endogenous level of RKS4 gene product was not changed. In the overexpressing plants 15.9 and 15.3 organ size was increased, similar as the number of initiated leaf primordia.

Figure 9

Arabidopsis thaliana WS plants in which the endogenous level of RKS4 gene product is decreased (right picture) due to the presence of a transgenic RKS4 antisense construct (GT-RKS4-16a). The left picture shows a wildtype plant of the same age as the transgenic antisense plant, grown under similar growth conditions. Plant size, organ size and number of organ primordia is decreased in the transgenic antisense plant compared with the wildtype control.

Figure 10

Arabidopsis thaliana WS plants in which the endogenous level of RKS4 gene product is decreased (bottom left picture) due to the presence of a transgenic RKS4 antisense construct (GT-RKS4-16a). The upper right picture shows a wildtype flower of the same age as the transgenic antisense flower, grown under similar growth conditions. Total flower size is only slightly decreased in the transgenic antisense flower compared with the control flower, whereas organ size of petals is strongly decreased.

Arabidopsis thaliana WS plants in which the endogenous level of RKS4 gene product is increased (upper left picture) due to the presence of a transgenic RKS4 overexpressing construct (GT-RKS4-6s). Compared with the wildtype control flower, total flower size of the transgenic flower is clearly increased. Both sepal and petal organ size is clearly increased compared

with the control.
For comparison an *Arabidopsis thaliana* WS plant is shown which has been transformed with a construct encoding the GASA3 gene in sense direction, i.e. overexpressing GASA3.

Figure 11.
Formation of meristematic regions in the hypocotyl of *Arabidopsis thaliana* WS plants under influence of overexpression of RKS4.
RKS4 overexpression results in increases in flower and seed organ size that could be due to increase in cell elongation and/or cell division. In order to analyse the cell division patterns in plants with deregulated RKS4 expression the mitotic activity in transgenic plants was analyzed with the a unstable GUS reporter under the control of a cyclin B1;1 promoter (the Plant Journal 1999 (4) 503-508 Spatio-temporal analysis of mitotic activity with a labile cyclin-GUS fusion protein). *Arabidopsis thaliana* WS seedlings with the pCDG construct did not show gus activity (cell division) in hypocotyls (top) whereas the same pCDG line crossed with a constitutive RKS4 construct showed mitotic activity as indicated by GUS-positive cells (bottom); indicating that RKS4 overexpression activated mitotic activity in hypocotyls.

Figure 12
In *Arabidopsis thaliana* WS, the seed size is influenced by changing levels of RKS4 gene product. Constitutive overexpression of RKS4 results in increases in seed size (left) compared with control wildtype seeds (right). Antisense constitutive expression of RKS4 cDNA (middle)results in a decrease in seed size compared with the control (right). Magnification is identical in all photos as shown by the bar size.

Figure 13

Organ size can be influenced by either modulating cell division or cell elongation or a combination of both. In order to identify the total number of cells and the cell size within an organ the apical site of petals of mature *Arabidopsis* flowers was investigated. Petal organ size is clearly influenced by modulation of RKS4 gene product levels (bottom row for the flowers from which the apical petal epidermal cells were identified). Epidermal cell size is not changed in transgenic plants compared with the control.

Figure 14
Arabidopsis thaliana WS plants in which the endogenous level of RKS10 gene product is increased (right picture) due to the presence of a transgenic RKS10 overexpressing construct. The left picture shows the apical epidermus of a full grown cotyl from an empty vector transgenic seedling of the same age as the transgenic overexpressing cotyl, grown under similar growth conditions..

Figure 15
Arabidopsis thaliana WS plants in which the endogenous level of RKS10 gene product is decreased (right picture) due to the presence of a RKS10 antisense construct The left picture shows a wildtype plant of the same age as the transgenic antisense plant, grown under similar growth conditions. Plant size, organ size and number of organ primordia remains similar in both the transgenic antisense plants and the wildtype control.

Figure 16
In order to determine organ size variations in transgenic RKS10 transgenic plants compared with empty vector control transgenic plants (pGreen4K), flower organ size was determined of the four open flower stages of *Arabidopsis* inflorescences. The four successive flower stages are photographed under similar magnifications. No obvious changes in organ length could be observed in size of sepals, petals, stamen and carpel

between empty vector control flowers (pGreen4K), flowers with an antisense RKS10 construct (a) or plants overexpressing the RKS10 cDNA under the control of a 35S promoter (S

Figure 17
Tissue cultured auxin treated *transgenic Arabidopsis* T2 seedlings were grown on MS agar plates without hormones for a period of 3 weeks. Regeneration potential was scored and the formation and outgrowth of multiple shoot apical meristems from single seedling origin was displayed as (+). The formation and outgrowth of only one shoot apical meristem, leading to the formation of a normal rosette of leaves from individual plants was displayed as (-). Positive regeneration controls consisted of seedlings overexpressing either KNAT1, CUC2, IPT or cycD3. All of these showed an increase of regeneration capacity (+) compared with a negative control GUS overexpressing plant pGreen5K (-).
Representative examples of RKS and ELS cDNA overexpressing (s) or antisense (a) cosuppressing constructs in transgenic plants are shown in the bottom panels.

Figure 18.
Tobacco leaf discs were stably transformed with the RKS0 overexpressing construct GT-RKS0-23S and from a single transformation event, large numbers of regeneration plantlets were isolated and subcultured. All of the regenerated plants were potted and flowered. The original transformation event could be kept continuously in tissue culture indefinitely.

Figure 19
Seedlings from transgenic Arabidopsis thaliana containing either constructs overexpressing (s) or co-suppressing by antisense (a) the RKS gene products were screened for the appearance of fasciation. Several examples in which fasciation could be routinely observed are shown together with a negative control plant (pGreen5K, overexpressing the GUS gene) in which fasciation could never be observed.

Figure 20 - 23
Primary root tips of transgenic *Arabidopsis* plants (top rows) photographed under similar magnification. The bottom rows show the corresponding seedlings (also between each other under the same magnification). Figure 23 shows the specific *Arabidopsis* transgenes with a strong increase in root outgrowth.

Figure 24
Avarage root length of 10-30 transgenic *Arabidopsis* T2 seedlings from one T1 transgenic plant is shown.

Figure 25
T3 seedlings are shown from a strong co-suppressing RKS10 antisense construct line (T1-4; T2-6; T3 generation) and a strong overexpressing line (T1-4; T2-6; T3 generation). The overexpressing line is different and stronger from the one shown in Figure 4.1-4.5. Pictures are taken under similar magnifications.

Figure 26
T2 seed was germinated on horizontal MS agar plates and pictures were taken under similar magnification of representative examples of the lateral root development from transgenic RKS and ELS transgenic roots.

Figure 27
Pictures taken from transgenic RKS8 or RKS10 overexpressing roots taken directly behind the tip zone. Pictures are taken under same magnification.

Figure 28
Arabidopsis thaliana WS plants in which the endogenous level of RKS or ELS gene product is modified result in the formation of new meristem formation and / or outgrowth, resulting in a complex, bushy inflorescence in transgenic *Arabidopsis* plants compared with control empty vector control plants (pGreen4K).

Overexpression of RKS10 and ELS1 (S) and cosuppression with antisense constructs of RKS8 and also RKS10, result in increased numbers of developing generative meristems. The generative shoots are photographed with similar magnification.

Figure 29

Arabidopsis thaliana WS plants in which the endogenous level of RKS gene product is modified result in the formation of new meristem formation and / or outgrowth, resulting in a complex, bushy inflorescence in transgenic *Arabidopsis* plants conmpared with control empty vector control plants (pGreen4K). The top panel shows adult plants under similar magnification. Compared with the control, RKS10 overexpression results in an extreme bushy phenotypic plant. The results of co-suppressing the RKS8 gene product are less dramatic with respect to the bushiness. However, also in these transgenic plants the number of generative meristems is strongly increased compared with the control. The bottom panel shows the generative shoot in detail under similar magnification.

Figure 30

Schematic drawing of the different flower organs in an empty vector control pGreen4K flower (left) compared with a complex transgenic flower structure seen in transgenic *Arabidopsis* plants containing an antisense (a) RKS10 construct. The terminal flower meristem produces 2 sepals, 1 petal, 2 stamen, a carpel which is not a closed structure but open with groups of ovules on the inside and outside of this structure, and stigmatic cells protruding from the top part. Two new flowers are protruding from this structure, containing all flower organs in normal numbers.

Figure 31

Schematic drawing of the different flower organs in a complex transgenic flower structure seen in transgenic *Arabidopsis* plants T1-11 containing an antisense (a) RKS10 construct. The

terminal flower meristem produces 1 sepal, 2 petals, 2 stamen, a carpel which is not a closed structure but open with groups of ovules on the inside and outside of this structure, and stigmatic cells protruding from the top part. An undetermined flower meristem is protruding from the open carpel structure and forms a number of new flowers, including normal flowers (right) and another abnormal flower (left) which consists of a flower with half of the sepal, petal and stamen organs formed and a new terminal flower meristem protruding from this structure, developing in structures as seen in Figure 7.5. The stamen contain only small numbers of (viable) pollen compared with wildtype stamen (see also chapter 5).

Figure 32

Schematic drawing of the different flower organs in an empty vector control pGreen4K flower (left) compared with a complex transgenic flower structure seen in a transgenic *Arabidopsis* plant T1-11 containing an antisense (a) RKS10 construct (overview shown in Figure 7.4). The terminal flower meristem produces half the normal number of sepals, petals and stamen. The remaining part of the flower structure has converted into a new structure containing a new stem containing a single organ structure resembling a fusion between a petal and a sepal. On this structure several (viable) pollen grains can be observed.

Figure 33

Schematic drawing of the different flower organs in a complex transgenic flower structure seen in a transgenic *Arabidopsis* plant T1-12 containing an antisense (a) RKS10 construct. The terminal flower meristem originating from an undetermined generative meristem is here producing an axillary secondary undetermined meristem (left picture), a single organ resembling a stamen (bottom left), a normal flower and a terminal flower. This terminal flower structure contains 2 normal sepals, 2 normal petals, 2 normal stamen (with only a few viable pollen) and two organs resembling a fusion of

sepals /petals/stamen (see also figure 7.7). From this terminal flower structure two new flowers emerge (in a similar fashion as observed in Figure 7.3) containing normal numbers of flower organs (right photos). At the top of this figure a control inflorescense is shown schematically with terminal flower meristems as normally originate from the generative *Arabidopsis thaliana* generative meristem.

Figure 34

Schematic drawing and detailed pictures of several of the structures as shown in figure 7.6. At the right the organs resembling a fusion between sepals/petals/stamen are shown with viable pollen sticking out from these structures. At the top left the single stamen-like organ directly protruding from the main stem is shown.

Figure 35

Transgenic *Arabidopsis* plants overexpressing the RKS13 gene product show a modification of the normal flower inflorescence architecture, somewhat resembling the structures observed in RKS10 antisense plants. A terminal flower containing a normal seed developing silique and a small number of sepals, petals and stamen, develops at least 4 additional terminal flower meristems that develop abnormally themselves, resulting in open carpel structures and modifications of organ structures.

Figure 36

Transgenic plants in which the RKS and / or ELS genes are introduced behind a constitutive 35S promoter in an overexpressing (S) or antisense (a) configuration are analyzed for sterility and characterized further for defects in proper pollen development. As a negative control the normal pollen development of a transgene containing the empty expression vector (pG4K) was included. First generation transgenic flowers of RKS10 expressing constructs and second generation control vector and ELS2 are shown under similar magnification. In detail the stigmatic surface and surrounding stamen, are

shown under similar magnification, showing the presence or absence of pollen on the stamen or the stigmatic surface.

Detailed description

1.Modifying organ size

Plant size is determined by both cell elongation and cell division rate. Modifying either one or both processes results in a change in final organ size. Increasing the level of specific members of the family of RKS genes results in an increase in organ size, growth rate and yield. Modulating plant growth, organ size and yield of plant organs is the most important process to be optimized in plant performance. Here we show that modulating the level of members of the family of the RKS signaling complex is sufficient to modulate these processes. The invention provides herewith a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating cellular division during plant growth or organ formation, in particular wherein said gene comprises an RKS4 or RKJS 10 gene or functional equivalent thereof. Inactivation of endogenous RKS gene product results in a decrease in plant growth, proving that the normal function of these endogenous RKS gene products is the regulation of growth and organ size. Elevation of the levels of the regulating of the RKS signaling complex in plant cells is provided in order to increase:
the size of plant organs
the growth rate
the yield of harvested crop
the yield of total plant material
the total plant size

Decreasing the levels of endogenous RKS gene product is provided in order to decrease:
the size of plant organs

the growth rate
the total plant size

Results obtained (see also figures 6 to 13)

Overexpression and antisense constructs of full length RKS cDNA clones have been made under the control of 35S promoters. Transgenic plants have been produced in *Arabidopsis thaliana* and in *Nicotiana tabacum*. Subsequent generations of stably transformed plants were investigated for phenotypes and analyzed in detail. The phenotype observed in transgenic plants with antisense constructs of RKS4 (GT-RKS4-a) could be described as dwarf plants in which all plant organs showed a decrease in organs size and growth rate. Overexpression of RKS4 (GT-RKS4-s) resulted in plants with increased size of organs and an increase in growth rate Since cell size alone was not responsible for the modifications in organ size of petals it can be concluded that RKS4 is involved in the regulation of the cellular divisions during plant growth and organ formation. Overexpression of RKS 4 results in an increase of cellular divisions whereas a decrease in endogenous RKS 4 gene product levels within the plant results in a decrease of cellular division rates.

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2. Cell division

The mitotic cell cycle in eukaryotes determines the total number of cells within the organism and the number of cells within individual organs. The links between cell proliferation, cell differentiation and cell-cycle machinery are of primary importance for eukaryotes, and regulation of these processes allows modifications during every single stage of development. Here we show that modulating the level of members of the family of the RKS signaling complex is sufficient to modulate these processes. The invention provides herewith a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating cellular division during plant growth or organ formation, in particular wherein said gene comprises an RKS4 or RKJS 10 gene or functional equivalent Herewith the invention provides a method for modulating the number of cells to be formed within an eukaryotic organism as a whole or for modulating the cell number within individual organs is, which of primary importance in modulating plant developmental processes, especially of arable plants. Here we show that members of the RKS signaling complex are able to regulate the number of cellular divisions, thereby regulating the total number of cells within the organism or different organs.

Possible Applications

Elevation of the levels of the regulating RKS signaling complex members in plant cells in order to increase:
the size of plant organs
the growth rate
the yield of harvested crop
the yield of total plant material
the total plant size

Decreasing the levels of endogenous RKS signaling complex members in order to decrease:
the size of plant organs
the growth rate
the total plant size

Results obtained

Overexpression and antisense constructs of full length RKS cDNA clones have been made under the control of 35S promoters. Transgenic plants have been produced in *Arabidopsis thaliana* and in *Nicotiana tabacum*. Subsequent generations of stably transformed plants were investigated for phenotypes and analyzed in detail.

Overexpression of RKS 4 results in an increase of cellular divisions whereas a decrease in endogenous RKS 4 gene product levels within the plant results in a decrease of cellular division . Another example of RKS genes involved in cellular proliferation is provided by RKS10. Overexpression of RKS10 (S) results in a decrease in apical epidermal cells (Figure 14) compared with control plants containing an empty expression cassette (pGreen4K). Co-suppressing the endogenous RKS 10 gene in plants containing an antisense construct (a) showed clearly larger epidermal cells as the corresponding cells in wildtype control plants (Figure 15). In contrast to the plant phenotypes shown in RKS4 transgenic plants , no differences in plant or organ size could be observed in the RKS10 transgenic plants or organs. This shows that although the organ size remains constant, the number of cells within these organs is variable due to the differences in size of individual cells. These results indicate that normal RKS4 function within the plant can be described as an activator of cellular division.

Normal RKS10 function also involves an activation process on cellular division rate. This effect is also detectable in the root in the region directly behind the tip zone, where in the RKS10 overexpressing transgenes cellular divisions were

detectable in a region where normally cell proliferation has ceased. The plane of divisions of root cells in these transgenes is also clearly different from the normal plane of root cell division, resulting in clumps of cells with all types of division planes possible.

In contrast to RKS4, the final organ size in RKS10 transgenic plants is under the control of other organ size restriction processes, in such a way that the final organ volume remains constant (Figure 16). RKS4 and RKS10 are essentially involved in the same cell cycle activation process, but either addition organ size controlling functions of these RKS genes or the hierarchical order in which they regulate the cell cycle is different.

Literature

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3.Regeneration

Modification the levels of different RKS and ELS genes within plants allows the initiation and / or outgrowth of apical meristems, resulting in the formation of large numbers of plantlets from a single source. A number of gene products that is able to increase the regeneration potential of plants is known already. Examples of these are KNAT1, cycD3, CUC2 and IPT. Here we show that modulation of the endogenous levels of RKS genes results in the formation of new shoots and plantlets in different plant species like *Nicotiana tabacum* and *Arabidopsis thaliana*. herewith the invention provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein, allowing modulating apical meristem formation, in particular wherein said gene comprises an ELS1, RKS0, RKS3, RKS4, RKS8 or RKS10 gene or functional equivalent thereof. A direct application of a method according to the invention is the stable or transient expression of RKS and ELS genes or gene products in order to initiate vegetative reproduction. Regeneration can be induced after overexpression of for example RKS0 and ELS1; or by co-suppression of for example the endogenous RKS3, RKS4, RKS8 or RKS10 genes. Overexpression or co-suppression of these RKS and ELS gene products can be either transient, or stable by integration of the corresponding expression cassettes in the plant genome.

Results obtained

Overexpression and antisense constructs of full length RKS and ELS cDNA clones have been made under the control of 35S promoters. Transgenic plants have been produced in *Arabidopsis thaliana* and in *Nicotiana tabacum*. Subsequent generations of

stably transformed plants were investigated for phenotypes and analyzed in detail.

T2 transgenic seedlings of *Arabidopsis* were germinated in liquid MS medium supplemented with 1 mg/L 2,4-D for 1 week, followed by extensive washing and plating of the seedlings onto MS agar plates without hormones. Control transgenic seedstocks containing either a negative control vector (pGreen5K); or positive control overexpression constructs of gene products known to increase the regeneration potential (IPT, KNAT1, CUC2 and cycD3) were characterized for regeneration potential together with seedstocks from plants either overexpressing (s) or co-suppressing (a) all RKS and ELS gene products (Figure 17). Overexpression of the ELS1 and RKS0 cDNA clones resulted in an increase of shoot apical meristem formation and outgrowth, whereas antisense constructs (a) of these cDNA clones did not increase the regeneration potential (only increased regeneration results are shown). Antisense constructs of RKS3, RKS4, RKS8 and RKS10 also resulted in an increased formation and outgrowth of apical meristems (Figure 17).

T1 generation *Nicotiana tabacum* tissue cultures transformed with ELS and RKS gene products in either overexpression (s) cassettes or antisense co-suppression (a) cassettes allowed the regeneration of indefinite number of offspring plants from a single transformed cell origin (Figure 18). An example is shown for the overexpression of the GT-RKS0-23S construct. The resulting plants obtained from one transformation event in general showed no phenotypes. Only a subset of plants displayed RKS0 overexpression phenotypes (like loss of apical dominance and early flowering).

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4. Fasciation

Fasciation is normally a result from an increased size of the apical meristem in apical plant organs.
Modulation of the number of cells within the proliferating zone of the shoot apical meristem results in an excess number of cellular divisions, giving rise to excess numbers of primordia formed or to stems in which the number of cells is increased. The invention herewith provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating fasciation, in particular wherein said gene comprises an RKS0, RKS3, RKS8 or RKS10 gene or functional equivalent thereof. Here we for example show that modulation of the levels of RKS gene products in plants like *Arabidopsis thaliana* can result in fasciated stems as shown in Figure 19. A direct application as provided herein is the regulated formation of fasciation in plant species in which such a trait is desired like ornamental plants. Regulation of the initiation and extent of fasciation, either by placing the responsible RKS encoding DNA sequences under the control of stage or tissue specific promoters, constitutive promoters or inducible promoters results in plants with localized or constitutive fasciation of stem tissue. Another application is modulating the number of primordiae by regulation of the process of fasciation. An example is provided by for example sprouts, in which an increased number of primordia will result in an increased numbers of sprouts to be harvested. Fasciation can also result in a strong modification in the structural architecture of the inflorescence, resulting in a terminal group of flowers resembling the *Umbelliferae* type (an example is shown in Figure 19 where the fasciated meristem of a RKS0-7S *Arabidopsis* plant in which endogenous RKS0 gene product

levels have been deregulated clearly terminates in an *Umbelliferae* type inflorescence.

Results obtained

Overexpression and antisense constructs of full length RKS cDNA clones have been made under the control of 35S promoters. Transgenic plants have been produced in *Arabidopsis thaliana*. Subsequent generations of stably transformed plants were investigated for phenotypes and analyzed in detail. T2 transgenic seedlings of *Arabidopsis* were germinated on MS agar plates without hormones. Control transgenic seedstocks containing a negative control vector (pGreen5K) were tested for their ability to induce fasciation (Overexpression constructs (s) of RKS0, RKS8 and RKS10 cDNA clones resulted in fasciated plants, whereas antisense constructs (a) of these cDNA clones did not increase the regeneration potential (only positive results are shown). Antisense constructs of RKS3 gave also rise to fasciation (Figure 19).

Literature

-Functional domains in plant shoot meristems. U. Brand et al. 2001. Bioassays 23: 134-141.

-Dependence of stem cell fate in *Arabidopsis* on a feedback loop regulated by CLV3 activity.
U. Brand et al. 2000. Science 289: 617-619

5. Root development

Fasciation is normally a result from an increased size of the apical meristem in apical plant organs. Modulation of the number of cells within the proliferating zone of the root apical meristem results in an excess number of cellular divisions, giving rise to excess numbers of primordia formed or to roots in which the number of cells is increased. Adaptation to soil conditions is possible by regulation of root development of plants. Here we describe several processes in root development that can be manipulated by modification of the levels of the RKS signaling complex within the root. The invention provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating root development, in particular wherein said gene comprises an ELS1, ELS2, RKS1, RKS3, RKS4, RKS6 RKS8 or RKS10 gene or functional equivalent thereof. Root length, a result by either root cells proliferation or elongation, can for example be increased by overexpression of for example RKS3, RKS4, RKS6 and ELS2, or inactivation of the endogenous RKS10 gene product. Root length can also be decreased by decreasing of endogenous RKS1 levels or by strong overexpression of RKS10. The initiation of lateral roots is also regulated by RKS gene products. Overexpression of for example RKS10 can result in a strong increase in the initiation and outgrowth of lateral roots. Co-suppression of RKS1 also resulted in the initiation and outgrowth of large numbers of lateral roots. Root hair formation and elongation is important in determining the total contact surface between plant and soil. A strong increase of root hair length (elongation) can be obtained by overexpression of ELS1 and RKS3 gene products. As the roots of terrestrial plants are involved in the acquisition of water and nutrients, anchorage of the plant, synthesis of plant

hormones, interaction with the rhizosphere and storage functions, increasing or decreasing root length, for example for flexible adaptations to different water levels, can be manipulated by overexpressing or cosuppressing RKS and / or ELS gene products. Modulation of the total contact surface between plant cells and the outside environment can be manipulated by regulation lateral root formation (increased by RKS10 overexpression and co-suppression of RKS1). Finally the contact surface between plant cells and the soil can be influenced by modulation of the number of root hairs formed or the elongation of the root hairs, as mediated by ELS1 and RKS3.

Results obtained

Overexpression and antisense constructs of full length RKS cDNA clones have been made under the control of 35S promoters. Transgenic plants have been produced in *Arabidopsis thaliana*. Subsequent generations of stably transformed plants were investigated for phenotypes and analyzed in detail. T2 transgenic seedlings of *Arabidopsis* were germinated on MS agar plates without hormones. Control transgenic seedstocks containing a negative control vector pGreen4K (empty expression vector) and / or pGreen5K (a GUS overproducing vector) were included as references for normal root development. Seedlings from transgenic Arabidopsis thaliana containing either constructs overexpressing (s) or co-suppressing by antisense (a) the RKS gene products were screened for the appearance of fasciation. Several examples in which fasciation could be routinely observed are shown together with a negative control plant (pGreen4K, containing an expressing cassette without an insert cDNA). Seedlings are germinated and grown on vertically placed MS agar plates.

Literature

-Cellular organisation of the *Arabidopsis thaliana* root. L. Dolan et al. 1993. Development 119: 71-84
-Root development in *Arabidopsis*: four mutants with dramatically altered root morphogenesis. P.N. Benfey et al. 1993. Development 119: 57-70
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6. Apical meristems

All parts of the plant above the ground are generally the result on one apical shoot meristem that has been initiated early at embryogenesis and that gives rise to all apical organs. This development of a single meristem into complex tissue and repeated patterns is the result of tissue and stage-dependent differentiation processes within the meristems and its resulting offspring cells. The control of meristem formation, meristem identity and meristem differentiation is therefore an important tool in regulating plant architecture and development. Here we present evidence the function of RKS and ELS gene products in regulation of the meristem identity and the formation and outgrowth of new apical meristems. The invention provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating meristem identity, in particular wherein said gene comprises an ELS1, RKS8, RKS10 or RKS13 gene or functional equivalent thereof. Introduction of for example the RKS10 gene product or an other member of the RKS signaling complex under the control of a tissue and / or stage specific promoter as provided herein allows localized and time regulated increases in the levels of gene product. For example the meristematic identity in a determined meristem might thereby be switched back into an undetermined meristem, thereby changing for example a terminal flower into an undetermined generative meristem.

Another application might be found in changing the meristematic identity at an early time point, during early vegetative growth, thereby switching the vegetative meristem into a generative meristem, allowing early flowering.

Modulation of meristem identity in terminal primordia, like for example as shown in Figure 30, where flower organ primordia are converted into terminal flower primordia, allows

the formation of completely new types of flowers and fused fruit structures. Constitutive overexpression of RKS gene products results in plants with many apical meristems, as can clearly been seen in Figure 29, where RKS10 overexpression results in an extremely bushy phenotype.

Results obtained

Changing the normal levels of endogenous RKS10 within the plant, either by overexpressing or co-suppressing the RKS10 cDNA, results in an increase in generative meristem development (Figure 28).

Compared with the control empty vector transgenic pGreen4K plants, large number of meristems are initiated at places were normally no meristems initiate and / or develop. A clear example is shown by co-suppressing the RKS8 gene (Figure 29), where many new inflorescence meristems are initiated from the central generative meristem compared with control pGreen4K plants of the same age. This phenotype is even more extreme in RKS10 overexpressing plants where the resulting plants are extremely bushy with very large numbers of generative meristems formed. Inactivation of the endogenous RKS10 gene in *Arabidopsis* results in modification of meristematic identity as can be shown in Figure 30. A determined flower meristem develops into two new normal terminal flower meristems and a number of terminal flower organ primordia. Another example is shown in Figure 31 where meristem determination is switched from a terminal flower meristem, that normally result only in the normal numbers of terminal organ primordia, towards a number of organ primordia, a new undetermined generative meristem that develop into normal flowers or in a new terminal flower meristem with developmental abnormalities. Only half of the terminal flower primordia develop normally while an extra structure arises resembling a new flower stem with a petal/stamen like organ. The few pollen detectable on this structure (Figure 32) were able to pollinate a MS1 (male sterile) *Arabidopsis* flower. Figure 33 shows the meristematic

developmental switch from a terminal flower meristem into a new undetermined generative meristem, that gives rise to a new formation of another undetermined meristem, and several normal and abnormal terminal flowers. The abnormal flowers again show the fusion of different structures, in this case from sepals, petals and stamen together (Figure 34). Surprisingly, directly on the generative stem another structure, resembling a single stamen was detectable. All these data indicate that a decrease in RKS1 expression levels results in switches in the meristematic identity. Meristems can switch forward and backward between developmental stages, indicating that RKS10 is normally involved in regulating the meristematic identity and the developmental order of meristematic development. RKS13 seems to be involved in similar processes, as can be concluded from the switches in flower meristematic outgrowths observed in figure 35. Modification of the expression levels of RKS1 also results in modified meristem identity. Suppression of endogenous RKS1 levels results in a developmental switching of generative meristems towards vegetative meristems, together with other phenotypes (results not shown).

Literature

-To be, or not to be a flower-control of floral meristem identity. H. Ma 1998. Trends in Genetics 14: 26-32

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7. Male sterility

Male sterility is a highly desired trait in many plant species. For example, manipulation of pollen development is crucial for F1 hybrid seed production, to reduce labour costs and for the production of low-environmental impact genetically engineered crops. In order to produce hybrid seed from inbred plant lines, the male organs are removed from each flower, and pollen from another parent is applied manually to produce the hybrid seed. This labour-intensive method is used with a number of vegetables (e.g. hybrid tomatoes) and with many ornamental plants. Transgenic approaches, in which one or more introduced gene products interfere with normal pollen initiation and development is therefore highly desired. Especially when the number of revertants (growing normal pollen) is extremely low.

Male sterility in plants is a desired trait that has been shown already in many plant species as a result of the inactivation of expression of a number of genes essential for proper stamen development, mitotic divisions in the pollen stem cells, or male gametogenesis. A method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein, allowing modulating pollen development, in particular wherein said gene comprises an ELS2 or RKS10 gene or functional equivalent thereof.

Here we present data that show that overexpression of gene products, like transmembrane receptor kinases (RKS) and extracellular proteins (ELS) can also result in the formation of male sterility. The ability to induce male sterility by overexpressing specific genes as provided herein allows the opportunity to produce transgenic overexpressing plants in which the pollen development is inhibited. Stable single copy homozygous integration of such overexpressing traits into the

plant genome will render such plants completely sterile, making them excellent material for the production of F1 hybrid seed. Furthermore, the combined integration of a male sterility inducing overexpressing gene coupled directly with another desired transgene result in transgenic plants which are unable to produce transgenic seed, making these transgenic plants excellent material for outside growth without problems affecting transgenic pollen spreading throughout the environment, thereby eliminating possible crosses with wild plant species or other non-transgenic crops. The combination of a desired transgene flanked on both sites by different male-sterility inducing overexpressing genes would decrease the frequency of pollen formation to an extremely low level. An example is an overexpressing construct of RKS10 at the 5'end of integrated DNA fragment, the desired transgene expression cassette in the middle and at the 3'end of the integrated DNA the ELS2 overexpressing construct. This complete DNA fragment is integrated into the genome by conventional techniques, like particle bombardment, *Agrobacterium* transformation etc. Another possible application concerns the modification of pollen in ornamental plant species like lily, where the release of pollen from cut flowers can be avoided by making transgenic plants in which pollen development is initiated by release from the stamen is prevented (a desired trait that can be obtained by overexpressing for example ELS2, resulting in partial pollen development). Hereby the ornamental value of the stamen with pollen is not lost, but release of pollen is inhibited.

Results obtained

Overexpression and antisense constructs of full length RKS cDNA clones have been made under the control of 35S promoters. Transgenic plants have been produced in *Arabidopsis thaliana*. Subsequent generations of stably transformed plants were investigated for phenotypes and analyzed in detail. T2 transgenic seedlings of *Arabidopsis* were germinated on MS agar plates without hormones. Control transgenic plants

containing a negative control vector pGreen4K (empty expression vector) were included as references for normal stamen and pollen development. RKS10 and ELS2 resulted in sterile plants when overexpressed in *Arabidopsis*. Antisense RKS10 plants resulted in a strong reduction in the number of pollen formed (Figure 36). In order to determine whether pollen development itself was the reason for sterility (and not a combination of pollen developmental mutants coupled to either embryo lethals or female gametogenesis defects), reciprocal crosses were performed between sterile transgenic plants and wildtype *Arabidopsis thaliana* WS plants. These results confirmed that the sterile plants with overexpressing RKS10 and ELS2 constructs were male sterile but completely female fertile. No defects could be observed in embryo development from crosses between female transgenic overexpressors and male wildtype pollen (results not shown). Since both antisense and overexpressing constructs of the RKS10 gene showed defects in proper pollen development we conclude that normal levels of endogenous RKS10 gene product are essential for proper pollen formation, outgrowth and differentiation. In the ELS2 overexpressing plants the initiation of pollen grains was not inhibited. However the proper development of pollen grains in full grown viable pollen was clearly inhibited .

Literature

-The *Arabidopsis* male sterility1 (MS1) gene is a transcriptional regulator of male gametogenesis, with homology to the PHD-finger family of transcription factors. Wilson et al. 2001. the Plant Journal 28: 27-39

-Transposon tagging of a male sterility gene in *Arabidopsis*. Aarts et al. 1993. Nature 363: 715-717

8. Resistance mechanisms

Two-hybrid interaction experiments have already shown *in vitro* interaction between RKS and NDR0-NHL and members of the SBP/SPL family. Here we show that *in vivo* the individual components of this signalling cascade are regulating identical processes, as based on functional genomics on transgenics plants, overexpressing or co-suppressing single components or combinations of components in this transmembrane signalling complex.

Here we show a large number of new members of the NDR/NHL gene family and we postulate a function as syntaxins in the pathogen resistance:

At2g27080;
MAERVYPADS PPQSGQFSGN FSSGEFPKKP APPPSTYVIQ VPKDQIYRIP PPENAHRFEQ
LSRKKTNRSN CRCCFCSFLA AVFILIVLAG ISFAVLYLIY RPEAPKYSIE GFSVSGINLN
STSPISPSFN VTVRSRNGNG KIGVYYEKES SVDVYYNDVD ISNGVMPVFY QPAKNVTVVK
LVLSGSKIQL TSGMRKEMRN EVSKKTVPFK LKIKAPVKIK FGSVKTWTMI VNVDCDVTVD
KLTAPSRIVS RKCSHDVDLW **

At5g21130
MTVEKPQEMT GDTNSDGFLT NKDVHRIKHP SLDTNDSSSS RYSVDSQKSR IGPPPGTYVI
KLPKDQIYRV PPPENAHRYE YLSRRKTNKS
CCRRCLCYSL SALLIIIVLA AIAFGFFYLV
YQPHKPQFSV SGVSVTGINL TSSSPFSPVI RIKLRSQNVK GKLGLIYEKG NEADVFFNGT
KLGNGEFTAF KQPAGNVTVI VTVLKGSSVK LKSSSRKELT ESQKKGKVPF GLRIKAPVKF
KVGSVTTWTM TITVDCKITV DKLTASATVK TENCETGLSL L*

At1g65690
MSQHQKIYPV QDPEAATARP TAPLVPRGSS RSEHGDPSKV PLNQRPQRFV PLAPPKKRRS
CCCRCFCYTF CFLLLLVVAV GASIGILYLV FKPKLPDYSI DRLQLTRFAL NQDSSLTTAF
NVTITAKNPN EKIGIYYEDG SKITVWYMEH QLSNGSLPKF YQGHENTTVI YVEMTGQTQN
ASGLRTTLEE QQQRTGNIPL RIRVNQPVRV KFGKLKLFEV RFLVRCGVFV DSLATNNVIK
IQSSSCKFRL RL*

At5g36970
MSDHQKIHPV SDPEAPPHPT APLVPRGSSR SEHGDPTKTQ QAAPLDPPRE KKGSRS
CWCRCVCYTLLVLF LLIVIVGAIV GILYLVFRPK FPDYNIDRLQ LTRFQLNQDL
SLSTAFNVTI
TAKNPNEKIG IYYEDGSKIS VLYMQTRISN GSLPKFYQGH ENTTIILVEM TGFTQNATSL
MTTLQEQQRL TGSIPLRIRV TQPVRIKLGK LKLMKVRFLV RCGVSVDSLA ANSVIRVRSS
NCKYRFRL*

At1g54540
MGDQQKIHPV LQMEANKTKT TTPAPGKTVL LPVQRPIPPP VIPSKNRNMC CKIFCWVLSL
LVIALIALAI AVAVVYFVFH PKLPSYEVNS LRVTNLGINL DLSLSAEFKV EITARNPNEK
IGIYYEKGGH IGVWYDKTKL CEGPIPRFYQ GHRNVTKLNV ALTGRAQYGN TVLAALQQQQ
QTGRVPLDLK VNAPVAIKLG NLKMKKIRIL GSCKLVVDSL STNNNINIKA SDCSFKAKL*

At5g06320

MADLNGAYYG PSIPPPKKVS HSHGRRGGGC GCLGDCLGCC GCCILSVIFN ILITIAVLLG
IAALIIWLIF RPNAIKFHVT DAKLTEFTLD PTNNLRYNLD LNFTIRNPNR RIGVYYDEIE
VRGYYGDQRF GMSNNISKFY QGHKNTTVVG TKLVGQQLVL LDGGERKDLN EDVNSQIYRI
DAKLRLKIRF KFGLIKSWRF KPKIKCDLKV PLTSNSTSGF VFQPTKCDVD F**

At5g11890
MTDRVFPASK PPTATNGAPP VGSIPPPPAP ATVTSNGTTN GMANQKPQVY IPANRPVYRP
QPYSRRHHHQ SRPSCRRICC CCCFWSILII LILALMTAIA ATAMYVIYHP RPPSFSVPSI
RISRVNLTTS SDSSVSHLSS FFNFTLISEN PNQHLSFSYD PFTVTVNSAK SGTMLGNGTV
PAFFSDNGNK TSFHGVIATS TAARELDPDE AKHLRSDLTR ARVGYEIEMR TKVKMIMGKL
KSEGVEIKVT CEGFEGTIPK GKTPIVATSK KTKCKSDLSV KVWKWSF*

At1g17620
MTDDRVYPAS KPPAIVGGGA PTTNPTFPAN KAQLYNANRP AYRPPAGRRR TSHTRG
CCCRCCCWTIFVII LLLLIVAAAS AVVYLIYRPQ RPSFTVSELK ISTLNFTSAV
RLTTAISLSV
IARNPNKNVG FIYDVTDITL YKASTGGDDD VVIGKGTIAA FSHGKKNTTT LRSTIGSPPD
ELDEISAGKL KGDLKAKKAV AIKIVLNSKV KVKMGALKTP KSGIRVTCEG IKVVAPTGKK
ATTATTSAAK CKVDPRFKIW KITF**

At3g11650
MGSKQPYLNG AYYGPSIPPP PKAHRSYNSP GFGCCCFSCL GSCLRCCGCC ILSLICNILI
AVAVILGVAA LILWLIFRPN AVKFYVADAN LNRFSFDPNN NLHYSLDLNF TIRNPNQRVG
VYYDEFSVSG YYGDQRFGSA NVSSFYQGHK NTTVILTKIE GQNLVVLGDG ARTDLKDDEK
SGIYRINAKL RLSVRFKFWF IKSWKLKPKI KCDDLKIPLG SSNSTGGFKF QPVQCDFDLS**

At2g22180
MEGPRRPPSA TAPDSDDDKP DDPPSVWHRP TSSLPALPSL DPPSHGSHHW RNHSLNLSPL
PTTSSPPLPP PDSIPELETY VVQVPRDQVY WTPPPEHAKY VEKRSKNPEK NKKKGCSKRL
LWFFIILVIF GFLLGAIILI LHFAFNPTLP VFAVERLTVN PSNFEVTLRA ENPTSNMGVR
YMMEKNGVVS LTYKNKSLGS GKFPGLSQAA SGSDKVNVKL NGSTKNAVVQ PRGSKQPVVL
MLNMELKAEY EAGPVKRNKE VVVTCDVKVK GLLDAKKVEI VSENCESEFK N*

At5g22870
MCHKPKLELM PMETSPAQPL RRPSLICYIF LVILTLIFMA AVGFLITWLE TKPKKLRYTV
ENASVQNFNL TNDNHMSATF QFTIQSHNPN HRISVYYSSV EIFVKFKDQT LAFDTVEPFH
QPRMNVKQID ETLIAENVAV SKSNGKDLRS QNSLGKIGFE VFVKARVRFK VGIWKSSHRT
AKIKCSHVTV SLSQPNKSQN SSCDADI*

At2g35980
MAAEQPLNGA FYGPSVPPPA PKGYYRRGHG RGCGCCLLSL FVKVIISLIV ILGVAALIFW
LIVRPRAIKF HVTDASLTRF DHTSPDNILR YNLALTVPVR NPNKRIGLYY DRIEAHAYYE
GKRFSTITLT PFYQGHKNTT VLTPTFQGQN LVIFNAGQSR TLNAERISGV YNIEIKFRLR
VRFKLGDLKF RRIKPKVDCD DLRLPLSTSN GTTTTSTVFP IKCDFDF**

At2g46300
MADYQMNPVL QKPPGYRDPN MSSPPPPPPP IQQQPMRKAV PMPTSYRPKK KRRSCCRFCC
CCICITLVLF IFLLLVGTAV FYLWFDPKLP TFSLASFRLD GFKLADDPDG ASLSATAVAR
VEMKNPNSKL VFYYGNTAVD LSVGSGNDET GMGETTMNGF RQGPKNSTSV KVETTVKNQL
VERGLAKRLA AKFQSKDLVI NVVAKTKVGL GVGGIKIGML AVNLRCGGVS LNKLDTDSPK
CILNTLKWYK IISN*

At4g05220
MTPDRTTIPI RTSPVPRAQP MKRHHSASYY AHRVRESLST RISKFICAMF
LLVLFFVGVI AFILWLSLRP HRPRFHIQDF

VVQGLDQPTG VENARIAFNV TILNPNQHMG VYFDSMEGSI YYKDQRVGLI
PLLNPFFQQP TNTTIVTGTL TGASLTVNSN RWTEFSNDRA QGTVGFRLDI
VSTIRFKLHR WISKHHRMHA NCNIVVGRDG LILPKFNHKR CPVYFT*

At2g35460
MANGLNGASY GPPIKPPVKT YYSHGRRGSD VGCGICGCFS SCLLCCGGCL VNIICNILIG
VLVCLGVVAL ILWFILRPNV VKFQVTEADL TRFEFDPRSH NLHYNISLNF SIRNPNQRLG
IHYDQLEVRG YYGDQRFSAA NMTSFYQGHK NTTVVGTELN GQKLVLLGAG GRRDFREDRR
SGVYRIDVKL RFKLRFKFGF LNSWAVRPKI KCHLKVPLST SSSDERFQFH PTKCHVDL*

At2g27260
MQDPSRPATG YPYPYPYPNP QQQQPPTNGY PNPAAGTAYP YQNHNPYYAP QPNPRAVIIR
RLFIVFTTFL LLLGLILFIF FLIVRPQLPD VNLNSLSVSN FNVSNNQVSG KWDLQLQFRN
PNSKMSLHYE TALCAMYYNR VSLSETRLQP FDQGKKDQTV VNATLSVSGT YVDGRLVDSI
GKERSVKGNV EFDLRMISYV TFRYGAFRRR RYVTVYCDDV AVGVPVSSGE GKMVGSSKRC
KTY**

At4g01410
MGEGEAKAEH AAKADHKNAP SASSTPESYS KEGGGGGGDA RRAICGAIFT ILVILGIIAL
ILWLVYRPHK PRLTVVGAAI YDLNFTAPPL ISTSVQFSVL ARNPNRRVSI HYDKLSMYVT
YKDQIITPPL PLPPLRLGHK STVVIAPVMG GNGIPVSPEV ANGLKNDEAY GVVLMRVVIF
GRLRWKAGAI KTGRYGFYAR CDVWLRFNPS SNGQVPLLAP STCKVDV*

At5g22200
MTGRYCDQHN GYEERRMRMM MRRIAWACLG LIVAVAFVVF LVWAILHPHG PRFVLQDVTI
NDFNVSQPNF LSSNLQVTVS SRNPNDKIGI FYDRLDIYVT YRNQEVTLAR LLPSTYQGHL
EVTVWSPFLI GSAVPVAPYL SSALNEDLFA GLVLLNIKID GWVRWKVGSW VSGSYRLHVN
CPAFITVTGK LTGTGPAIKY QLVQRCAVDV *

At1g61760
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ILWISLQPHR PRVHIRGFSI SGLSRPDGFE TSHISFKITA HNPNQNVGIY YDSMEGSVYY
KEKRIGSTKL TNPFYQDPKN TSSIDGALSR PAMAVNKDRW MEMERDRNQG KIMFRLKVRS
MIRFKVYTWH SKSHKMYASC YIEIGWDGML LSATKDKRCP VYFT*

At3g52470
MSKDCGNHGG GKEVVVRKLC AAIIAFIVIV LITIFLVWVI LRPTKPRFVL QDATVYAFNL
SQPNLLTSNF QVTIASRNPN SKIGIYYDRL HVYATYMNQQ ITLRTAIPPT YQGHKEVNVW
SPFVYGTAVP IAPYNSVALG EEKDRGFVGL MIRADGTVRW KVRTLITGKY HIHVRCQAFI
NLGNKAAGVL VGDNAVKYTL ANKCSVNV**

At5g53730
MSQISITSPK HCAKKGGINI NNRHKKLFFT FSTFFSGLLL IIFLVWLILH PERPEFSLTE
ADIYSLNLTT SSTHLLNSSV QLTLFSKNPN KKVGIYYDKL LVYAAYRGQQ ITSEASLPPF
YQSHEEINLL TAFLQGTELP VAQSFGYQIS RERSTGKIII GMKMDGKLRW KIGTWVSGAY
RFNVNCLAIV AFGMNMTTPP LASLQGTRCS TTI*

At4g01110
MAGETLLKPV LQKPPGYREL HSQPQTPLGS SSSSSSMLRR PPKHAIPAAF YPTKKRQWSR
CRVFCCCVCI TVAIVILLLI LTVSVFFLYY SPRLPVVRLS SFRVSNFNFS GGKAGDGLSQ
LTAEATARLD FRNPNGKLRY YYGNVDVAVS VGEDDFETSL GSTKVKGFVE KPGNRTVVIV
PIKVKKQQVD DPTVKRLRAD MKSKKLVVKV MAKTKVGLGV GRRKIVTVGV TISCGGVRLQ
TLDSKMSKCT IKMLKWYVPI QVKCI*

At2g35960
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NLSQPNLLTS NFQITIASRN RNSRIGIYYD RLHVYATYRN QQITLRTAIP PTYQGHKEDN
VWSPFVYGNS VPIAPFNAVA LGDEQNRGFV TLIIRADGRV RWKVGTLITG KYHLHVRCQA
FINLADKAAG VHVGENAVKY MLINKCSVNV *

At3g52460
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PPYPNYPNAP YQQYPYAQAP PASYYGSSYP AQQNPVYQRP ASSGFVRGIF TGLIVLVVLL
CISTTITWLV LRPQIPLFSV NNFSVSNFNV TGPVFSAQWT ANLTIENQNT KLKGYFDRIQ
GLVYHQNAVG EDEFLATAFF QPVFVETKKS VVIGETLTAG DKEQPKVPSW VVDEMKKERE
TGTVTFSLRM AVWVTFKTDG WAARESGLKV FCGKLKVGFE GISGNGAVLL PKPLPCVVYV*

At4g09590
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FNLSQPNLLT SKFQITIASR NRNSNIGIYY DHLHAYASYR NQQITLASDL PPTYQRHKED
SVWSPLLYGN QVPIAPFNAV ALGDEQNSGV FTLTICVDGQ VRWKVGTLTI GNYHLHVRCQ
AFINQADKAA GVHVGENTVK YTLINKCSVN F*

At2g35970
MTTKECGNHG GGGGGGGTAC RICGAIIGFI IIVLMTIFLV SIILQPKKPE FILQDTTVYA
FNLSQPNLLT SKFQITIASR NRNSNIGIYY DHLHAYASYR NQQITLASDL PPTYQRHKEN
SVWSPLLYGN QVPIAPFNAV ALGDEQNSGV FTLTICVDGR VRWKVGTLTI GNYHLHVRCQ
AFINQADKAA GVHVGENTVK YTLINKCSVN F*

At3g26350
MSHHHHHETN PHFARIPSQN PHLKSGGAST SQTSSNQPHI PPIPHPKKSH HKTTQPHPVA
PPGILIKTRG RHRENPIQEP KHSVIPVPLS PEERLPPRKT QNSSKRPLLL SPEDNQQQRP
PPPQAPQRNG GGYGSTLPPI PKPSPWRTAP TPSPHHRRGP RLPPPSRETN AMTWSAAFCC
AIFWVILILG GLIILIVYLV YRPRSPYVDI SAANLNAAYL DMGFLLNGDL TILANVTNPS
KKSSVEFSYV TFELYYYNTL IATQYIEPFK VPKKTSMFAN VHLVSSQVQL QATQSRELQR
QIETGPVLLN LRGMFHARSH IGPLFRYSYK LHTHCSVSLN GPPLGAMRAR RCNTKR*

At3g11660
MKDCENHGHS RRKLIRRIFW SIIFVLFIIF LTILLIWAIL QPSKPRFILQ DATVYAFNVS
GNPPNLLTSN FQITLSSRNP NNKIGIYYDR LDVYATYRSQ QITFPTSIPP TYQGHKDVDI
WSPFVYGTSV PIAPFNGVSL DTDKDNGVVL LIIRADGRVR WKVGTFITGK YHLHVKCPAY
INFGNKANGV IVGDNAVKYT FTTSCSVSV**

At3g44220
MTEKECEHHH DEDEKMRKRI GALVLGFLAA VLFVVFLVWA ILHPHGPRFV
LQDATIYAFN VSQPNYLTSN LQVTLSSRNP NDKIGIFYDR LDIYASYRNQ
QVTLATLLPA TYQGHLDVTI WSPFLYGTTV PVAPYFSPAL SQDLTAGMVL
LNIKIDGWVR WKVGTWVSGR YRLHVNCPAY ITLAGHFSGD GPAVKYQLVQ RCAVDV*

At1g08160
MVPPNPAHQP ARRTQPQLQP QSQPRAQPLP GRRMNPVLCI IVALVLLGLL VGLAILITYL
TLRPKRLIYT VEAASVQEFA IGNNDDHINA KFSYVIKSYN PEKHVSVRYH SMRISTAHHN
QSVAHKNISP FKQRPKNETR IETQLVSHNV ALSKFNARDL RAEKSKGTIE MEVYITARVS
YKTWIFRSRR RTLKAVCTPV MINVTSSSLD GFQRVLCKTR L**

At2g01080
MPPPPSSSRA GLNGDPIAAQ NQQPYYRSYS SSSSASLKGC CCCLFLLFAF LALLVLAVVL
IVILAVKPKK PQFDLQQVAV VYMGISNPSA VLDPTTASLS LTIRMLFTAV NPNKVGIRYG
ESSFTVMYKG MPLGRATVPG FYQDAHSTKN VEATISVDRV NLMQAHAADL VRDASLNDRV
ELTVRGDVGA KIRVMNFDSP GVQVLLPSFL PAFCSLSDLA *

At5g06330

MTSKDCGSHD SHSSCNRKIV IWTISIILLL ILVVILLVWA ILQPSKPRFV LQDATVFNFN
VSGNPPNLLT SNFQFTLSSR NPNDKIGIYY DRLDVYASYR SQQITLPSPM LTTYQGHKEV
NVWSPFVGGY SVPVAPYNAF YLDQDHSSGA IMLMLHLDGR VRWKVGSFIT GKYHLHVRCH
ALINFGSSAA GVIVGKYMLT ETCSVSV*

At5g56050
MSKFSPPPQS QPQPPETPPW ETPSSKWYSP IYTPWRTTPR STQSTPTTTP IALTEVIVSK
SPLSNQKSPA TPKLDSMEAH PLHETMVLLQ LRTSRTNPWI WCGAALCFIF SILLIVFGIA
TLILYLAVKP RTPVFDISNA KLNTILFESP VYFNGDMLLQ LNFTNPNKKL NVRFENLMVE
LWFADTKIAT QGVLPFSQRN GKTRLEPIRL ISNLVFLPVN HILELRRQVT SNRIAYEIRS
NFRVKAIFGM IHYSYMLHGI CQLQLSSPPA GGLVYRNCTT KRW*

At3g20600
NDR1
MNNQNEDTEG GRNCCTCCLS FIFTAGLTSL FLWLSLRADK PKCSIQNFFI PALGKDPNSR
DNTTLNFMVR CDNPNKDKGI YYDDVHLNFS TINTTKINSS ALVLVGNYTV PKFYQGHKKK
AKKWGQVKPL NNQTVLRAVL PNGSAVFRLD LKTQVRFKIV FWKTKRYGVE VGADVEVNGD
GVKAQKKGIK MKKSDSSFPL RSSFPISVLM NLLVFFAIR*

At3g54200
MSDFSIKPDD KKEEEKPATA MLPPPKPNAS SMETQSANTG TAKKLRRKRN CKICICFTIL
LILLIAIVIV ILAFTLFKPK RPTTTIDSVT VDRLQASVNP LLLKVLLNLT LNVDLSLKNP
NRIGFSYDSS SALLNYRGQV IGEAPLPANR IAARKTVPLN ITLTLMADRL LSETQLLSDV
MAGVIPLNTF VKVTGKVTVL KIFKIKVQSS SSCDLSISVS DRNVTSQHCK YSTKL*

At3g20590
non-race specific disease resistance protein, putative
MTKIDPEEEL GRKCCTCFFK FIFTTRLGAL ILWLSLRAKK PKCSIQNFYI PALSKNLSSR
DNTTLNFMVR CDNPNKDKGI YYDDVHLTFS TINTTTTNSS DLVLVANYTV PKFYQGHKKK
AKKWGQVWPL NNQTVLRAVL PNGSAVFRLD LKTHVRFKIV FWKTKWYRRI KVGADVEVNG
DGVKAQKKGS KTKKSDSSLP LRSSFPIFVL MNLLVFFAIR *

At4g39740
MSHVTATSLA RFTKPVPKPA SSPIVNTKLT TSGGRTAAFM DLSSFRLTVW
DPDTANDSSG KFPWPRFLFF FLTLKTGGSG LNIKPTISAI AQMMNPMTIT
EMNNQMHRLE QKLLLFLPGS LFLRLSTILH YPGEGSNRPD PLEHALRRSR
SLGLDQEEAA KKVIRVGRDS KNDYVNVVEN QAASFLRRCG PSKRIQSVNY
CKSTRQGHEI PDVKPLFPTG GGTQAPSRSR ARYAVPAILL GFAGFVGFLH
YNDERRAVPR GQASSNSGCG CGSNTTVKGP IIGGPFTLVS TENKIVTEND
FCGKWVLLYF GYSFSPDVGP EQLKMMSKAV DKLAILLNPL TFGCLYLYAE
FDSRILGLTG TASAMRQMAQ EYRVYFKKVQ EDGEDYLVDT SHNMYLINPK
MEIVRCFGVE YNPDELSQEL LKEVASVSQ*

At1g32270 syntaxin, putative
MVRSNDVKFQ VYDAELTHFD LESNNNLQYS LSLNLSIRNS KSSIGIHYDR
FEATVYYMNQ RLGAVPMPLF YLGSKNTMLL RALFEGQTLV LLKGNERKKF
EDDQKTGVYR IDVKLSINFR VMVLHLVTWP MKPVVRCHLK IPLALGSSNS
TGGHKKMLLI GQLVKDTSAN LREASETDHR RDVAQSKKIA DAKLAKDFEA
ALKEFQKAQH ITVERETSYI PFDPKGSFSS SEVDIGYDRS QEQRVLMESR
RQEIVLLDNE ISLNEARIEA REQGIQEVKH QISEVMEMFK DLAVMVDHQG
TIDDIDEKID NLRSAAAQGK SHLVKASNTQ GSNSSLLFSC SLLLFFFLSG
DLCRCVCVGS ENPRLNPTRR KAWCEEEDEE QRKKQQKKKT MSEKRRREEK
KVNKPNGFVF CVLGHK*

At1g13050

MSHHHYETNP HFVQFSLQDQ HQGGPSSSWN SPHHHQIPQA HSVAPPRVKI KTRGRHQTEP
PETIHESPSS RPLPLRPEEP LPPRHNPNSA RPLQLSPEEQ RPPHRGYGSE PTPWRRAPTR
PAYQQGPKRT KPMTLPATIC CAILLIVLIL SGLILLLVYL ANRPRSPYFD ISAATLNTAN
LDMGYVLNGD LAVVVNFTNP SKKSSVDFSY VMFELYFYNT LIATEHIEPF IVPKGMSMFT
SFHLVSSQVQ IQMIQSQDLQ LQLGTGPVLL NLRGTFHARS NLGSLMRYSY WLHTQCSISL
NTPPAGTMRA RRCNTKR*

At5g45320
MPRLTSRHGT SPFIWCAAII CAIISIVVIV GGIIVFVGYL VIHPRVPIIS
VADAHLDFLK YDIVGVLQTQ LTIVIRVEND NAKAHALFDE TEFKLSYEGK
PIAILKAPEF EVVKEKSMFL PYLVQSYPIP LNPTMMQAVD YAVKKDVITF
ELKGGSRTRW RVGPLGSVKF ECNLSCQLRF RPSDHSYIPS PCTSAHKH*

At3g20610
MDRDDAWEWF VTIVGSLMTL LYVSFLLALC LWLSTLVHHI PRCSIHYFYI PALNKSLISS
DNTTLNFMVR LKNINAKQGI YYEDLHLSFS TRINNSSLLV ANYTVPRFYQ GHEKKAKKWG
QALPFNNQTV IQAVLPNGSA IFRVDLKMQV KYKVMSWKTK RYKLKASVNL EVNEDGATKV
KDKEDGIKMK ISDSSPQRLT FFQVCFSIIC VLMNWLIFLA IR*

At4g26490
MVLTKPATVR FNGLDAEPRK DRVILRQPRS SRTSLWIWCV AVFLAIRPRI PVFDIPNANL
HTIYFDTPEF FNGDLSMLVN FTNPNKKIEV KFEKLRIELF FFNRLIAAQV VQPFLQKKHE
TRLEPIRLIS SLVGLPVNHA VELRRQLENN KIEYEIRGTF KVKAHFGMIH YSYQLHGRCQ
LQMTGPPTGI LISRNCTTKK *

At5g42860
MHAKTDSEVT SLSASSPTRS PRRPAYFVQS PSRDSHDGEK TATSFHSTPV
LTSPMGSPPH SHSSSSRFSK INGSKRKGHA GEKQFAMIEE EGLLDDGDRE
QEALPRRCYV LAFIVGFSLL FAFFSLILYA AAKPQKPKIS VKSITFEQLK
VQAGQDAGGI GTDMITMNAT LRMLYRNTGT FFGVHVTSSP IDLSFSQITI
GSGSIKKFYQ SRKSQRTVVV NVLGDKIPLY GSGSTLVPPP PPAPIPKPKK
KKGPIVIVEP PAPPAPVPMR LNFTVRSRAY VLGKLVQPKF YKRIVCLINF
EHKKLSKHIP ITNNCTVTSI *

At1g45688
MHAKTDSEVT SLAASSPARS PRRPVYYVQS PSRDSHDGEK TATSFHSTPV LSPMGSPPHS
HSSMGRHSRE SSSSRFSGSL KPGSRKVNPN DGSKRKGHGG EKQWKECAVI EEEGLLDDGD
RDGGVPRRCY VLAFIVGFFI LFGFFSLILY GAAKPMKPKI TVKSITFETL KIQAGQDAGG
VGTDMITMNA TLRMLYRNTG TFFGVHVTST PIDLSFSQIK IGSGSVKKFY QGRKSERTVL
VHVIGEKIPL YGSGSTLLPP APPAPLPKPK KKKGAPVPIP DPPAPPAPVP MTLSFVVRSR
AYVLGKLVQP KFYKKIECDI NFEHKNLNKH IVITKNCTVT TV*

At4g26820
MDDEQNLVEE MNQQLLITVI DTEKVPELRP ISSRSHQESE PANISHWSLL FKLFLAITIM
GACVAGVTFV ILITPTPPTV HVQSMHISFA NHNLPVWSAT FSIKNPNEKL HVTYENPSVW
LVHRGKLVST ARADSFWQKG GEKNEVIVKR NETKVIDEEA AWEMEDEVAV TGGVVGLDMV
FSGRVGFYPG TSALWGEQYM SAVCENVSAK LYNVDDEIYG TNRSVLSFDG RLVCSVRLPK
YP*

Plants respond in a variety of ways to pathogens. After a recognition of the pathogen, normally mediated by avr and R genes, the resulting response induces a hypersensitive

response, that results in inhibition of the pathogen. After the recognition, further processes appear to be non-specific. In addition to the hypersensitive response, a second line of defence, defined as the systemic acquired resistance response can be triggered, that renders unaffected parts of the plant resistant to a variety of normally virulent pathogens. Several of the RKS and ELS gene products prove to be key regulators in the regulation of the system acquired resistance response.

Overexpression of several of the RKS and / or ELS genes in plants, either by constitutive promoters, stage and / or tissue specific promoters, or inducible promoters allows the activation of a systemic acquired resistance response in plants.

Another application can be provided by the activation of a RKS /ELS specific ligand in (transgenic) plants, thereby activating the receptor complex, that finally results in triggered activation of the systemic acquired resistance response in these plants.

(ref. Generation of broad-spectrum disease resistance by overexpression of an essential regulatory gene in systemic acquired resistance. H. Cao et al. 1998. Proc. Natl. Acad. Sci. USA 95: 6531-6536). Recent literature shows the functional interaction between RKS10 and BRI-1, another class of transmembrane LRR receptor kinases (Cell Vol. 110, 213-222 2002). BAK1=RKS10 as descibed here, interacts with BRI-1 and modulates brassinosteroid signaling; Cell vol 110, 203-212 2002 BRI1/BAK1 a receptor kinase pair mediating brassinosteroid signaling). Brassinosteroids are known to function in a broad range of disease resistance in tobacco and rice (Plant Journal 2003, 887-898). The BRI-1 receptor is involved in the binding of systemin, an 18 amino acid polypeptide, representing the primary signal for the systemic activation of defence genes (PNAS 2002, 9585-9590).

ELS overexpression phenotypes mimic the effects of inactivation of RKS molecules gene products. Either ELS is competing for ligand binding, or ELS inhibits the interactions

between RKS and BRI-1-like gene products. ELS1 overexpression results in dwarf phenotypes in Arabidopsis and tobacco plants, similar as observed for antisense RKS4 and RKS10, and for knock out plants of RKS0 and RKS4.

Deregulating expression of ELS and / or RKS genes in plant would modify the broad spectrum disease resistance in such plants. This would explain the observed data that brassinosteroids are involved in disease resistance (Plant Journal 2003, 33 887-898.)

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